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	ates/sec
	Search time 3927 Seconds (without alignments) 9966.580 Million cell updates/sec
OM nucleic - nucleic search, using sw model	April 30, 2004, 14:44:42 ; Search time 3927 Seconds (without alignments) 9966.580 Million cell upo
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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No.	Score	e Match	Length	ВВ	ΙD	Description
	6	100.		9	AR308734	8734 S
7	903	100.		9	AX549189	189
	903	100.		φ.	AX675043	5043 Seque
4° U	903	- ·		on 0	AF024687	<u>, </u>
n w	, 6	0 0	•	, 4	AR308751	ARAOR751 Semience
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21	33	3 2		ο ω	AK140313 E41325	E41325 CDNA Clone
22	21.	13		9	AR308737	AR308737 Sequence
23	121.8	Ξ:		9	AX224754	AX224754 Sequence
24 25	7.5	1 -		o u	AX224756	AX224756 Sequence
26	2:	13		9	AF024688	AF024688 Homo sapi
27	21.	13		6	AF024689	AF024689 Homo sapi
28	2 2	13	٠	ο (BC035657	BC035657 Homo sapi
30	18.	13	"	n vo	ACCOZSII AR308752	ACOUZELL HUMAN DNA AR308752 Semience
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32		σ.		9	BD137966	BD137966 Protease-
33		σ σ	1534	o 4	AF080214	AF080214 Homo sapi
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36			4895	9	AR242695	AR242695 Sequence
37			4895	9	AX549230	AX549230 Sequence
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					ALIGNMENTS	
RESULT 1	4					
LOCUS		AR308734				linear PAT 12-JUN-2003
DEFINITION			249 from	from patent	US 6555339	
VERSION		AK308/34 AR308734.:	1 GI:31	7002	.63	
KEYWORDS		Unknown				
ORGANISM	Σ	Unknown.	70			
REFERENCE AUTHORS		(bases	o 9	903) m, D.P.	and Chalmers, D.T.	
TITLE		Non-endogenou receptors	e,	const	itutively activated	human protein-coupled
JOURNAL	_	tent: US	S 655533	4-6	249 29-APR-2003;	

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Mammalia, Euthería, Prímates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                          Burmer,G.C., Roush,C.L. and Brown,J.P.
Antigenic peptides, such as for G protein-coupled receptors (GPCRs), antibodies thereto, and systems for identifying such antigenic peptides
Patent: WO 02061087-A 474 08-AUG-2002;
Lifespan Biosciences, Inc. (US)
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.5e-132;
Matches 903; Conservative 0; Mismatches 0;
                                                      Sequence 474 from Patent W002061087. AX549189
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 1.5e-132;
Matches 903; Conservative 0; Mismatches 0; Indels
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43 A3	\$ A	è 8	& 8	& 8	8 8 8	성 a r	g	\$ B	oy Oy	& 4 6	& 8	S S	RES AFO LOC	DEF ACC VER	SOS	REF	E D
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Danganan,L., Bruce,R., Quan,G., Montgomery,M., Ow,D., Kobayashi,A.,
Olsen,A.O. and Carrano,A.V.
Sequence analysis of a 1 Mb region in human 19913.1
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Lamerdin,J.B., McCready,P., Adamson,A.W., Burkhart-Schultz,K.,
Garcia,E., Kyle,A., Ramirez,M., Stilwagen,S., Garnes,J.,
Banganan,L., Bruce,R., Quan,G., Montgomery,M., Ow,D., Kobayashi,A.,
Olsen,A.O. and Carrano,A.V.
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B-cell receptor CD22-A isoform (CD22) gene, complete cds, complete
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Genomic structure and chromosomal mapping of the human CD22 gene
J. Immunol. 150 (11), 5013-5024 (1993)
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Wilson, G.L., Najfeld, V., Kozlow, E., Menniger, J., Ward, D. and
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J. Exp. Med. 173 (1), 137-146 (1991)
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GRYLGAAFPLGYQAPRRFCYSMGVCAALWALVI.CHLGLVFGLBAPGGWLDHSNTSLGI
PYNGSPYCLEAWDPASAGPAFFSLSILLIFFIPLAITAFCYVGCLRALARSGI.THRR
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ilarity 100.0%; Pred. No. 1.5e-132;
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O'Dowd, B.F.
Direct Submission
Submitted (15-SEP-1997) Department of Toronto, 8 Taddle Creek Rd., Toronto, Location/Qualifiers
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/organism="Homo sapiens"
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from hybrid UVSHL9-58, which carries chromosome 19 as its
only human chromosome"
n complement(128. .279)
//note="88# similarity"
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                                                                                                                    Direct Submission
Submitted (14-NOV-2002) DOB Joint Genome Institute, 2800 Mitchell
Submitted (14-NOV-2002) DOB Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Nov 7, 2002 this sequence version replaced gi:1498644.
NOTE: This insert is not the entire sequence of the clone (entire sequence is 40kb). It is clipped at the overlap with AC002511. The number of bases overlapped is 6888.
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join(637). 6570,7043. 7420,10532. 10837,12251. 12517,
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19325. 19421,19547. 19622,20098. .20216,20647. .20731,
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Drive, Walnut Creek, CA 94598, USA
6 (bases 1 to 34791)
DOB Joint Genome Institute and Stanford Human Genome Center.
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complement (5422. .5707)
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TVOILHSPAVEGSOVEFLORILANDLETNYTWYHNGKEMOGETEEKVHIPEKILEWHAG
TYSCVARNILGTGORGPGAELDVOYPPKKYTYTVIONPMPIREDTYTLECHYNSSNPS
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                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 903)
Liaw,C.W., Behan,D.P. and Chalmers,D.T.
Non-endogenous, constitutively activated
                                                                                                                                                               DNA
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Patent: US 655339-A 271 29-APR-2003;
Location/Qualifiers
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/mol_type="genomic DNA"
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Sequence 271 from patent US 6555339.
AR308751
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/translation="MOLPPQDSFALYVSAFALGFPLNLLAIRGAVSHAKLRLFPSLVY
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Method of screening for gpr40 ligands
Patent: WO 02057783-A 3 25-JUL-2002;
Glaxo Group Limited (GB); Smithkline Beecham

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GRYLGAAFPFGYQAVRRPRYSMGVCVAIWALVLCHMGLVLGIBAPGGWLNTTSSSLGI
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KLRAMMAAGGAFLTLLLCLGFPVNASIVVASFVNPDLGGSWRKLGLITGSWSVVLNFLVT
GYLGASPGRGTVCTTRTQGGTIQK"
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/protein_id="BAC82556.1"
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/translation="MALSPQLPFALYVSAFALGFPLNLLAIRGAVARARLRLTPNLVY
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (08-NOV-2002) Shuji Hinuma, Discovery Research Laboratorises I, Takeda Chemical Industries, Ltd.; Wadai 10, Tsukuba, Ibaraki 300-4293, Japan (8-mail:Hinuma_Shuji@takeda.co.jp, Tel:81-298-64-5035, Fax:81-298-64-5000)
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Sciurognathi; Muridae; Cricetinae;
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Direct Submission
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Kobayashi, W., Fuljii, K., Fukusumi, S., Tanaka, Y., Maruyama, M.,
Uejima, H., Satoh, K., Kizawa, H., Okubo, S., Ogi, K., Komatsu, H.,
Matsumura, F., Noguchi, Y., Fukatsu, K., Hinuma, S., Fujisawa, Y..
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ROD 02-SEP-2003

linear

AB095745 903 bp mRNA Mus musculus mRNA for GPR40, complete cds. AB095745

RESULT 10
AB095745
LOCUS
DEFINITION
ACCESSION

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GYLGTGPGRGTICVTRTQRGTIQK"
                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (08-NOV-2002) Shuji Hinuma, Discovery Research
Laboratories 1, Takeda Chemical Industries, Ltd., Wadai 10,
Tsukuba, Ibaraki 300-4293, Japan (E-mail:Hinuma_Shuji@takeda.co.jp,
Tel:81-298-64-5035, Fax:81-298-64-5000)
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Shoji, F., Shoichi, O., Noguchi, Y., Itoh, Y., Kobayashi, M., Fujii, R. and Hinuma, S.
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                                                                                                     Itoh,Y., Hosoya,M., Harada,M., Kawamata,Y., Tanaka,H.,
Kobayashi,M., Fujii,R., Fukusumi,S., Tanaka,Y., Maruyama,M.,
Uejima,H., Satoh,R., Kizawa,H., Okubo,S., Ogi,K., Komatsu,H.,
Matsumura,F., Noguchi,Y., Fukatsu,K., Hinuma,S., Fujisawa,Y.
Fujino,M.
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                                                                                                                                                                                                                   Expression of GPR40 in pancreatic cells Unpublished
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(house
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Mammalia; Eutheria;
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Andrews, J. L., Briscoe, C.P., Ignar, D.M., Muir, A.I., Sauls, H.R. Jr. and Tadayyon, M. Escening for GRR40 Ligands
Patent: PCT WO/02/05/783-B 25-JUL-2002;
Glaxo Group Limited, Glaxo Wellcome House, Berkely Avenue;
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Briscoe, C.P., Tadayyon, M., Andrews, J.L., Benson, W.G.,
Chambers, J.K., Eilert, M.M., Ellis, C., Elshourbagy, N.A., Goetz, A.,
Mindock, D.T., Mirdock, P.R., Sauls, H.R. Jr., Shabon, U.,
Spinage, L.D., Strum, J.C., Szekeres, P.G., Tan, K.B., Way, J.M.,
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The orphan G protein-coupled receptor GPR40 is activated by mediand long-chain fatty acids
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                                                                    TGCTACGTGGGCTGCCTCCGGGCACTGGCCCGCTCCGGCCTGACGCACAGGCGGAAGCTG
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                                                 AACACCGGTCAACGGCTCTCCGGTCTGCCTGGAGGCCTGGGACCCGGCCTCTGCCGGC
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Submitted (01-AUG-2002) Metabolic Diseases, GlaxoSmithKline,
Moore Drive, Durham, NC 27709, USA
Location/Qualifiers
1. 1819
/organism="Mus musculus"
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Mus musculus GPR40 (Gpr40) gene, complete cds.
AF539809
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Ellis, C. and Elshourbagy, N.
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musculus
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181655: gap of unknown length
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/db_xref="texon:10090"
/clone="R23-2229"
/clone_lib="RPCI mouse BAC library 23"
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Consensus quality: 180765 bases at least Q40
Consensus quality: 200208 bases at least Q30
Estimated insert size: 207873; sum-of-contigs estimation
Quality coverage: 8.28 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
consists of 21 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N. but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
                                                                                                                       HTG 09-DEC-2000
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1195 AGGGCAGCTTGGGTGGCCGGAGGCGCTCTCCTCACACTCCTGCTCTGCCTGGGGGCCCTAT 125
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Submitted (09-DEC-2000) Production Sequencing Pacility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                  AC087143 209873 bp DNA linear HTG 09-DEC-200
Mus musculus clone RP23-22G9, WORKING DRAFT SEQUENCE, 21 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 2088)
DOB Joint Genome Institute.
                                                                                                                                                                         841 AGGGGTCCTGGCCTGAAGACAGTGTGTGCGGCAAGAACGCAAGGGGGCAAGTCCCAGAAG
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1953: gap of unknown length
2957: contig of 1004 bp in length
3057: gap of unknown length
4549: contig of 1492 bp in length
649: gap of unknown length
6366: contig of 177 bp in length
6466: gap of unknown length
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Center clone name: RPCI-23_22G9
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Center: Joint Genome Institute
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AC087143.1 GI:11610869
HTG; HTGS PHASE1; HTGS_DRAFT.
Mus musculus (house mouse)
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DOE Joint Genome Institute.
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Submitted (02-SEP-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
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DOB Joint Genome Institute.
Sequencing of Mouse
Unpublished
2 (bases 1 to 154673)

DOB Joint Genome Institute.
GTCTTTGGGTTGGAGGCTCCAGGAGGCTGGCTGGACCACAGCAACACCTCCCTGGGCATC
                                                                                     106687 AACATACCCGTGAATGGCTCCCCGGTCTGCCTGGAAGCCTGGGATCCCGACTCTGCCCGC
                                                                                                                                                                                                        TGCTACGTGGGCTGCCTCCGGGCACTGGCCCGCCTCCGGCCTGACGCACAGGCTG
                                                                  AACACACCGGTCAACGGCTCTCCGGTCTGCCTGGAGGCCTGGGACCCGGCCTCTGCCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.jgi.doe.gov
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HTG; HTGS PHASE1; HTGS DRAFT.
Mus musculus (house mouse)
Mus musculus
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AC079472
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Quality coverage: 9.04 in Q20 bases; agarose-fp estimation Quality coverage: 13.25 in Q20 bases; sum-of-contige estimation.

**NOTE: This is a "working draft" sequence. It currently consists of 34 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
                                                                                                                                  as soon as it is available and the accession number will be preserved.
Estimated insert size: 151373; sum-of-contigs estimation
                                                                                                                                                                                             contig of 1439 bp in length
contig of 1439 bp in length
contig of 1158 bp in length
contig of 1158 bp in length
contig of 1189 bp in length
contig of 1185 bp in length
gap of unknown length
contig of 1185 bp in length
contig of 11855 bp in length
contig of 1555 bp in length
contig of 1781 bp in length
contig of 1781 bp in length
contig of 1781 bp in length
contig of 2249 bp in length
contig of 2249 bp in length
contig of 1781 bp in length
contig of 1781 bp in length
gap of unknown length
contig of 1781 bp in length
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gap of unknown length
contig of 6349 bp in length
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contig of 9815 bp in length
gap of unknown length
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gap of unknown l
contig of 2401 b
gap of unknown l
gap of unknown l
contig of 2971 b
gap of unknown l
contig of 1551 b
gap of unknown l
contig of 4528 b
gap of unknown l
contig of 4694 b
gap of unknown l
contig of 4828 b
gap of unknown l
contig of 4694 b
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gap of unknown
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gap of unknown length
contig of 6860 bp in length
contig of 5610 bp in length
contig of 5611 bp in length
gap of unknown length
contig of 6900 bp in length
gap of unknown length
contig of 12384 bp in length
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Submitted (08-NOV-2002) Shuji Hinuma, Discovery Research
Laboratories 1, Takeda Chemical Industries, Ltd.; Wadai 10,
Tsukuba, Ibaraki 300-4293, Japan (E-mail:Hinuma_Shuji@takeda.co.jp,
Tel:81-298-64-5035, Fax:81-298-64-5000)
Location/Qualifiers
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Sciurognathi; Muridae; Murinae;
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Shoji,F., Shoichi,O., Noguchi,Y., Itoh,Y., Kobayashi,M., Fujii,R.
and Hinuma,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and
                                                                      CCATTGAACTTGTTAGCCATCCGAGGGGGGGGGGGGGAAACTGGGGACTCACCCCC
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Kobayashi,M., Fujii,R., Fukusumi,S., Tanaka,Y., Maruyama,M.,
Uejima,H., Satoh,R., Kizawa,H., Okubo,S., Ogi,K., Komatsu,H.,
Matsumura,F., Noguchi,Y., Fukatsu,K., Hinuma,S., Fujisawa,Y.
                                    894
                                    841 AGGGTCCTGGCCTGAAGACAGTGTGTGCGCCAAGAAGGCAAGGGGGCCAAGTCC
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Rattus norvegicus mRNA for GPR40, complete cds.
AB095744
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/db_xref="taxon:10116"
1. .903
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Rodentia;
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Best Local Similarity 78.4%;
Matches 707; Conservative
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114272 AGCTTGGTCTACTCTCCATCTGGGCTGCTCTGATCTCCTACTGGCCATCACTCTGCCC 114331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGAAGGCTGTGGAGGCCCTGGTTCTGGAGCCTGGCCCCTGCCGCTCCCCTTCTGCCCA 114391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114392 GTCTTTGCCTTGGCCCACTTTGCTCCCCTCTACGCAGGCGGAGGCTTCCTAGCTGCTCT 114451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGCCTGGTCTACGCCCTGAACCTGGGCTGCTCCGACCTGCTGACAGTCTCTCTGCCC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u> AGTGCAGGCCGCTACCTGGGAGCAGCCTTCCCCTTGGGCTACCAAGCCTTCCGGAGGCCG</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                 66.2%; Score 598; DB 2; Length 154673; llarity 79.3%; Pred. No. 4.4e-85; Conservative 0; Mismatches 185; Indels 0;
132993: contig of 8927 bp in length
133093: gap of unknown length
142772: contig of 9679 bp in length
142872: gap of unknown length
154673: contig of 11801 bp in length.
                                                                                                                                                                                                       /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="RP3-123923"
/clone_lib="RPCI mouse BAC library 23"
                                                                                                                                                  Location/Qualifiers
1. .154673
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                           132994
133094
142773
142873
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Matches 709;
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/protein_id="AaN03479.1"
/db_xref="G1:22597184"
/db_xref="G1:22597184"
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NIPWGSPVCLEAWDPDSARPARLSFSILLFFLPLVITAFCYVGCLRALVHSGLSHKR
KIRRAWVAGGALLTLLCLGCPYNASFINPDLEGGSWRKIGLITGAWSVVLNPLVT
GYLGTGPGGGTICVTRTPRGTIQK"
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Best Local Similarity 78.4%; Pred. No. 2.3e-83;
Matches 707; Conservative 0; Mismatches 195; Indels
                                                                                                                                                                                      1. .907
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
1. .907
                     The state of the s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="GPR40"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           codon_start=1
                                                                                                                                                                                                                                                                                                                                         /gene="Gpr40"
5. .907
                                                                                                                                                                                                                                                                                                                                                                                                  /gene="Gpr40"
/note="GPCR"
                                                                                                                                                                                                                                                                                                                                                                          .907
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The orphan G protein-coupled receptor GPR40 is activated by medium and long-chain fatty acids
J. Eilert acids
J. Eilert Strum, J. J. 11303-11311 (2003)
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Rattus norvegicus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
AGGGCAGCTTGGGTGGGTGGAGCACTTCTCTCACACTCTGCTCTGCCTGGGGCCCTAT
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AF539810.1 GI:22597183
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Ellis,C.E. and Elshourbagy,N.
Rat GPR40 cDNA
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US-10-202-687-1 903 Title: Perfect score:

1 atggacctgccccgcagct.......99gggcaagtcccagaagtaa 903 Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

3373863 segs, 2124099041 residues Searched:

6747726 Fotal number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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geneseqn1980s:* geneseqn1990s:*

geneseqn2000s:* geneseqn2001as:* geneseqn2001bs:* geneseqn2002s:* geneseqn2003as:*geneseqn2003bs:*geneseqn2003cs:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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STIMMARTES

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Result No.	Score	Query Match	Length	DB	ID	Description
-	903	001	903	-	33330759	To Committee Contract
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7	506	100.0		٥	ABK90236	Abk90236 Human CDN
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10	604.4	6.99	903	9	ABK90237	_
11	602.4	66.7	900	σ	ADB61401	Adb61401 DNA encod
12	588	65.1	900	0	ADB61403	Adb61403 DNA encod
13	123.4	13.7	1841	~	AAV53631	Aav53631 Human 7-t
14	121.8	13.5	1041	m	AAA30762	Aaa30762 Human G p
15	121.8	13.5	1041	4	AAH26460	Aah26460 Human G-p
16	121.8	13.5	1041	4	AAH26459	Aah26459 Human G-p
17	121.8	13.5	1041	7	ABZ42561	Abz42561 Human G p
18	121.8	13.5	1041	σ	ADC22772	Adc22772 Human G p
19	118.6	13.1	1041	m	AAA30777	Aaa30777 DNA encod
20	118.6	13.1	1041	σ	ADC22792	Adc22792 Human G p
21	84.6	9.4	1534	~	AAX90981	Aax90981 Human pro
22	84.6	9.4	1534	m	AAA35309	Aaa35309 Human ade
23	84.6	9.4	1534	m	AAF21431	Aaf21431 Human low

Human	Aaz32747 Human pro	Human	Abz42864 Human pro	Aah43632 Human PAR	Aaa35311 Human ade	Aaf21433 Human low	Abz97127 Human nuc	Aga30740 DNA encod	Aaa30666 Human G p	Abk48452 Human cDN	Aad50860 Human G-p	Abz42746 Human G p	Adc22744 Human G p	Adc22636 Human G p	Aas77014 DNA encod	Aas72718 DNA encod	Aas79030 DNA encod	Aas72235 DNA encod	Aav07250 DNA encod	Aas77311 DNA encod	Aas92500 DNA encod
ABZ97125	AAZ32747	AAZ50775	ABZ42864	AAH43632	AAA35311	AAF21433	ABZ97127	AAA30740	AAA30666	ABK48452	AAD50860	ABZ42746	ADC22744	ADC22636	AAS77014	AAS72718	AAS79030	AAS72235	AAV07250	AAS77311	AAS92500
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ALIGNMENTS

AAA30759 standard; cDNA; 903 BP. 21-AUG-2000 (first entry) AAA30759; RESULT 1 AAA30759

Human G protein-coupled receptor GPR40 cDNA.

G protein-coupled receptor; GPCR; constitutively active; intracellular loop 3; transmembrane domain 6; drug screening; agonist; antagonist; ss.

Homo sapiens.

WO200022129-A1.

20-APR-2000.

99WO-US023938 12-OCT-1999; 98US-00170496 13-OCT-1998;

(AREN-) ARENA PHARM INC

Liaw CW; Chalmers DT, Behan DP,

WPI; 2000-329165/28. P-PSDB; AAY90679.

Non-endogenous constitutively activated human G protein-coupled receptors, useful for identifying agonists for use as pharmaceutical agents.

Example 1; Page 307; 341pp; English.

The invention relates to constitutively active, non-endogenous versions of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-AAY90677 and AAY90681-Y90681-Y90680-YPO681-YPO681-YPO681-YPO681-YPO681-YPO8

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LUPA, and is preferably Lys. When the endogenous residue at this position is Lys, this residue is replaced by His, Arg or preferably Ala. The 15 amino acid stretch between the substituted amino acid and the Pro may be endogenous, non-endogenous, or a mixture of endogenous and non-endogenous considerable. The constitutively active GPCRs are useful for identifying antagonists, agonists and partial agonists for use as pharmaceutical companies. The mutant proteins are also useful in research settings for clucidating the roles of the receptors in normal and diseased and isoased conditions. Antagonists for a particular GPCR are useful for treating diseases and clisoates associated with that receptors. Because the novel mutant GPCRs are constitutively active, they can be used directly for screening of compounds without the need for endogenous ligands. The present sequence compounds without the need for endogenous ligands. The present sequence compounds without the need for endogenous ligands. The present council continuous hild cation of the invention. This was cloned and subjected to sitedirected mutagenesis (SDM) to generate DNA encoding the corresponding computant of the invention.
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Sequence 903 BP; 108 A; 327 C; 283 G; 185 T; 0 U; 0 Other;

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                                                         AGCCTGGTCTACGCCCTGAACCTGCTGCTGCTCCCGCTGCTGACAGTCTCTCTGCCC
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Score 903; DB 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to screening a test compound to determine whether the compound is a GPR40 receptor (G protein-coupled receptor) ligand comprises detecting whether the test compound competitively inhibits the binding of a fatty acid GRR40 ligand to a GPR40 receptor. Also included are (1) a method of screening a compound for GPR40 antagonist activity, comprising; (a) measuring any detectable signal produced by a reporter gene (comprising a reporter gene under the control of G protein Gq responsive transcriptional element); (b) detecting a decrease in reporter gene expression in the presence of both test compound and agonist; or (c) detecting whether the compound decreases glucose-stimulated insulin release from mammalian pancreatic beta cells in the presence of a GPR40 agonist; (2) a method of screening a compound for GPR40 agonist; (2) a method of screening any
                                                                                                                                  900
721 AACGCCTCCAACGTGGCCAGCTTCCTGTACCCCAATCTAGGAGGCTCCTGGCGGAAGCTG 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying GPR40 receptor ligand for treating disorders e.g. obesity, comprises detecting whether the test compound competitively inhibits the binding of a fatty acid GPR40 ligand to a GPR40 receptor.
                                                                                                                    841 AGGGGTCCTGGCCTGAAGACAGTGTGTGCGGCAAGAACGCAAGGGGGGAAGTCCCAGAAG
                                   GGGCTCATCACGGGTGCCTGGAGTGTGGTGCTTAATCCGCTGGTGACCGGTTACTTGGGA
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                                                                                                                                                                                                                                                                                                                                                                                     Human cDNA encoding G protein-coupled receptor GPR40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Page 44-48; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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/product= "GPR40"
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                                                                                                                                                                                                                                                                                     ABK90236 standard; cDNA; 903
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reporter gene expression; or (b) detecting whether the compound binds to GPR40 and increases glucose-stimulated insulin release from mammalian pancreatic beta cells. The method is useful for identifying GPR40 antagonist or agonist compounds for treating disorders e.g. type 2 diabetes, obesity, glucose or insulin intolerance, neurodegenerative disease (e.g. Alzheimer's disease) or stroke. The present sequence is the human cDNA for GPR40
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(LIFE-) LIFESPAN BIOSCIENCES INC.

Burmer GC, Roush CL, WPI; 2003-046718/04.

P-PSDB; ABP81994

19-DEC-2000; 2000US-0257144P. 19-DEC-2001; 2001WO-US050107

WO200261087-A2

08-AUG-2002.

sapiens

Homo

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G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; G protein-coupled receptor modulator; antibody; immune-related disease; growth-related disease; call regeneration-related disease; ADS; cancer; immunological-related cell proliferative disease; autoimmune disease; Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy; osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea; hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
                                                                                                                                Human G protein-coupled receptor GPR40 nucleotide SEQ ID NO:474.
                                                                      BP.
                                                                     ABZ42843 standard; DNA; 903
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New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or autoimmune diseases.

Disclosure, Fig 1; 523pp; English.

The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino caids. Also described: (I) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or articular GPCR. (I) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibody against a particular GPCR, and in the production of specific antibody. The peptides and antibodies are also useful for detecting the presence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for disquesting and antibodies are useful for disquesting and designing drugs for gresence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for disquesting and designing drugs for treating immune-related diseases, growth-related disease, call creating immune-related diseases, growth-related disease, call creating immune-related diseases, growth-related call proliferative diseases, or autoimmune diseases, growth-related call proliferative diseases, and allergies, corder, full and acute inflammation, allergies, crohn's disease, diabetes, graft versus host anxiety, depression, schizophrenia, dementia, mental retardation, memory closs, epilepsy, asthma, tuberculosis, obseity, nausea, hypertension, or hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or

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P-PSDB; ADC22769
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any other disorder in which GPCRs are involved. The antibodies may be used in immunoseasys and immunodiagnosis. ABZ42523 to ABZ42869 encode GPCR proteins given in ABP81675 to ABP82018, which are used in the exemplification of the present invention
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                                              Sequence 903 BP; 108 A; 327 C; 283 G; 185 T; 0 U; 0 Other;
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100.0%; Pred. No. 2e-167;
iive 0; Mismatches 0;
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The invention relates to a method for treating a non-endogenous, constitutively active version of an endogenous human G protein-coupled receptor (GFCR) that Lransmembrane-6 (TM6) region and an intracellular-3 (IC3) region, by substituting a specific amino acid in the TM6 region with a different amino acid, and testing for constitutive activity. The method is useful for creating a constitutively active version of an endogenous human GFCR that comprises a transmembrane 6 region and an intracellular loop 3 region. The altered human GFCR compounds for identification of inverse agonists or partial agonists of GPCR polypeptides, which may have therapeutic uses. The altered GPCRs may also be used in vivo or in vitro in biological research. A nucleic acid encoding the altered GPCR may be used to create a transgenic animal expressing the altered GPCR remay be used to create a transgenic animal expressing the altered GPCR. The method allows screening for compounds that modulate the activity of human G protein-coupled receptor without the need for provision of a cidentification of a creening of compounds against orbhan receptors for which no ligand is currently known. This sequence represents cDNA encoding a human GPCR currently known.
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                                                                                                                                                                                                                                                                                                                        Human; gene; ss; G protein-coupled receptor; GPCR;
transmembrane-6 region; TM6; intracellular-3 region; IC3.
                                                                                                                                                                                                                                            Human G protein-coupled receptor cDNA #36.
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ADC22768 standard; cDNA; 903
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antilipaemic; dermatological; antiarteriosclerotic; antiarthritic;

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The invention relates to a novel screening method comprising a fatty acid and eicosanoid-binding G-protein coupled receptor protein, GPR40, originating in mouse, rat, crab-eating monkey and hamster (sequences fully defined in the specification), equivalent proteins of similar activity, and peptides containing partial sequences of the GPR40 protein. The novel fatty acid and GPR40 protein and their compositions have the following activities: antidiabetic, anabolic, neuroprotective, nephrotropic, ophthalmological, antilipaemic, dermatological, enfiatorior, ophthalmological, antilipaemic, dermatological, antiatritic, osteopathic, thrombolytic, noctropic, anorectic, hypotensive, and cytostatic. The novel fatty acid and eicosanoid-binding G-protein coupled receptor protein, GPR40, and clarance, and else and else and be used in the treatment, prevention and diapetes, ketosis, acidosis, diabetic neuropathy, diabetic nephropathy, diabetic retinopathy, hyperlipaemia, skin diseases, confidence, insulin allergy, fat metabolism disorders and cancer. This confidence is insulin allergy, fat metabolism disorders and cancer. This
            osteopāthic; thrombolytīc; nootropic; anorectic; hypotensive; cytostatic; diabetes; ketosis; acidosis; diabetic neuropathy; diabetic nephropathy; diabetic retinopathy; hyporlipaemia; skin disease; arthritis; bone disease; arteriosclerosis; thromboslis; hyportrension; indigestion; memory loss; obesity; hypoglycaemia; edema; insulin resistance; insulin allergy; fat metabolism disorder; cancer; human; gene; ds.
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Y, Ogi K, Harada M, 1
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al Similarity 100.0%; Pred. No. 7.8e-167;
900; Conservative 0; Mismatches 0;
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12-JUL-2002; 2002JP-00204163.
12-NOV-2002; 2002JP-00328696.
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P-PSDB; ADB61404.
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                                                                                                                                      Homo sapiens.
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fatty acid; eicosanoid-binding G-protein coupled receptor; GPR40; antidiabetic; anabolic; neuroprotective; nephrotropic; ophthalmological;

DNA encoding human GPR40 protein.

(first entry)

04-DEC-2003

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ADB61405 standard; DNA; 900

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AAA30776 standard; DNA; 903 21-AUG-2000 AAA30776;

(first entry)

protein-coupled receptor; GPCR; constitutively active; ntracellular loop 3; transmembrane domain 6; drug screening; agonist; DNA encoding human mutant G protein-coupled receptor GPR40 (A223K)

Homo sapiens Synthetic.

WO200022129-A1

antagonist; mutant; 88.

Non-endogenous constitutively activated human G protein-coupled receptors, useful for identifying agonists for use as pharmaceutical Example 2; Page 324; 341pp; English. Liaw CW; 98US-00170496 Chalmers DT, (AREN-) ARENA PHARM INC WPI; 2000-329165/28. P-PSDB; AAY90684. 12-OCT-1999; Behan DP, agents.

The invention relates to constitutively active, non-endogenous versions of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-CAAY90647) and AAY90689-A30743 and AAY9077 and AAY9069-A30743 and AAA30775-A30779). The mutant proteins of the invention contain a contain a material and transmembrane domain 6 (TM6). A non-endogenous anino acid, X, is substituted for an endogenous residue in IC3 at a position 16 amino acids N-terminal of an endogenous residue in IC3 at a position 16 amino acids N-terminal of an endogenous proline in TM6 to form a sequence X-contains and is preferably Lys. When the endogenous residue at this position is Lys, this residue is replaced by His, Arg or preferably Ala. The 15 amino acid stretch between the substituted amino acid and the Pro may be endogenous, non-endogenous, or a mixture of endogenous and non-endogenous cresidues. The constitutively active GPCRs are useful for identifying antagonists for a particular gponists for use as pharmaceutical containment proteins are also useful in research settings for a particular GPCR are useful for treating diseases and disorders associated with that receptors. Because the novel mutant GPCRs are constitutively active, they can be used directly for screening of compounds without the need for endogenous ligands. Sequences AAA30709-CPC AMA30773 and AAA30779-FA30779 represent DNAs encoding the mutant human GPCRs of the invention

ö Length 903; Sequence 903 BP; 111 A; 325 C; 282 G; 185 T; 0 U; 0 Other; Indels Score 898.2; DB 3; Pred. No. 1.7e-166; 0; Mismatches 3; DB 3; 99.5%; Query Match
Best Local Similarity 99.7
Matches 900; Conservative 1 ATGGACCTGCCCCCCCCAGCTCTCCTTCCGCCTCTATGTGGCCCCCTTTGCCGCTGGGCTTC

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                    TGCTATTCCTGGGGGGTGTGCGCGCCCATCTGGGCCCTCGTCCTGTGTCACCTGGGTCTG
                                         GTCTTTGGGTTGGAGGCTCCAGGAGGCTGGACCACCACCAGCAACACCTCCCTGGCCATC
                                                                      AACACCCGGTCAACGGCTCTCCCGGTCTGCCTGCAGGCCTCGGGACCCGGCCTCTGCCGGC
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                                 AACACCGGTCAACGGCTCTCCGGTCTGCCTGGAGGCCTGGGACCCGGCCTCTGCCGGC
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98US-00060188.
98US-0090783P.
98US-0095677P.
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07-AUG-1998;
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The invention relates to a method for treating a non-endogenous, constitutively active version of an endogenous human G protein-coupled receptor (GFR) that has a transmembrane-6 (TM6) region and an intracellular-3 (IC3) region, by substituting a specific amino acid in the TM6 region with a different amino acid, and testing for constitutive curracellular-3 (IC3) region, by substituting a specific amino acid in the TM6 region with a different amino acid, and testing for constitutive activity. The method is useful for creating a constitutively active cursion of an endogenous human GPCR that comprises a transmembrane 6 region and an intracellular loop 3 region. The altered human GPCR polypeptides which may have therapeutic uses. The altered GPCRs may also be used to resten a transgenic animal expressing the altered GPCR. The wethor allows screening for compounds that modulate the activity of a human G protein-coupled receptor without the need for provision of a ligand for the receptor. This is particularly useful in allowing a currently known. This sequence represents cDNA encoding a human GPCR polypeptide of the invention.
Creating a constitutively active version of an endogenous human G protein coupled receptor (GPCR) comprises substituting a specific amino acid in the transmembrane-6 region with a different amino acid, and testing for
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                                                                                                                                                            Example 2; SEQ ID NO 271; 221pp; English
                                                                                               constitutive activity,
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541 CCGCCCCCCTTCAGCCTCTCTCTCTCTGTTTTTTTCTGCCCTTGCCCATCACAGCCTTC
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P-PSDB; ADB61416
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                   acid; eicosanoid-binding G-protein coupled receptor; GPR40;
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Y, Ogi K, Harada M, Fukusumi S;
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/note= "No stop codon"
/product= "Monkey GPR40 protein"
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12-JUL-2002; 2002JP-00204163.
12-NOV-2002; 2002JP-0028696.
22-JAN-2003; 2003JP-00014032.
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The invention relates to a novel screening method comprising a fatty acid and eicosanoid-binding G-protein coupled receptor protein, GPR40, coriginating in mouse, rat, crab-eating monkey and hamster (sequences tilly defined in the specification), equivalent proteins of similar activity, and peptides containing partial sequences of the GPR40 protein and their compositions have the following activities: antidiabetic, anabolic, neuroprotective, nephrotropic, ophthalmological, antilipaemic, dermatological, antiarteriosclerotic, hypotennive, and cytostatic. The novel fatty acid and eicosanoid-binding G-protein coupled receptor protein, GPR40, and further compositions can be used in the treatment, prevention and diagnosis of diabetes, ketosis, acidosis, diabetic retinopathy, hyperlipaemia, skin disease, carthritis, bone diseases, arteriosclerosis, thrombosis, hypertension, indigetion, memory loss, obesity, hypoglycaemia, edema, insulin resistance, insulin allergy, fat metabolism disorders and cancer. This protein of the invention.
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The invention relates to a novel screening method comprising a fatty acid and eicosanoid-binding G-protein coupled receptor protein, GPR40, originating in mouse, rat, crab-eating monkey and hamster (sequences fully defined in the specification), equivalent proteins of similar activity, and peptides containing partial sequences of the GPR40 protein. The novel fatty acid and GPR40 protein and their compositions have the following activities: antidiabetic, anabolic, neuroprotective, nephrotropic, ophthalmological, antilipaemic, dermatological, entiarteriosclerotic, antiarthritic, osteopathic, thrombolytic, nootropic, anorectic, hypotensive, and cytostatic. The novel fatty acid and eicosanoid-binding G-protein coupled receptor protein, GPR40, and clarance, anorectic, hypotensive, and cytostatic. The novel fatty acid and eicosanoid-binding G-protein coupled receptor protein, GPR40, and clarance compositions can be used in the treatment, prevention and classes, ketosis, acidosis, diabetic neuropathy, diabetic retinopathy, hyperlipaemia, skin diseases, carthritis, bone diseases, arteriosclerosis, thrombosis, hypertension, indigestion, memory loss, obesity, hypoglycaemia, skin disease, insulin allergy, fat metabolism disorders and cancer. This polymucleotide sequence represents the DNA encoding a hamster GPR40
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Pred. No. 1.5e-110;
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Best Local Similarity 80.07
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Kawamata Y, Ogi K, Harada M,
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/product= "Hamster GPR40 protein"
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12-NOV-2002; 2002JP-00328696.
22-JAN-2003; 2003JP-00014032.
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                                                                       781 GGCTCATCACAGGCTCCTGGAGTGTGGTACTCAACCCGCTGGTCACCGGTTACTTGGGA
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GPR40 and increases glucose-stimulated insulin release from mammalian pancreatic beta cells. The method is useful for identifying GPR40 antagonist or agonist compounds for treating disorders e.g. type 2 diabetes, obesity, glucose or insulin intolerance, neurodegenerative disease (e.g. Alzheimer's disease) or stroke. The present sequence is mouse cDNA for GPR40
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                                                                                                                                                                            Sequence 903 BP; 138 A; 300 C; 245 G; 220 T; 0 U; 0 Other;
                                                                                                                                                                                                                        Score 604.4; DB 6;
Pred. No. 4.5e-109;
0; Mismatches 186;
                                                                                                                                                                                                                          Query Match
Best Local Similarity 79.4%;
Matches 716; Conservative
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Matches 714,
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                                                                                                                                                                                                  fatty acid; eicosanoid-binding G-protein coupled receptor; GPR40; antidiabetic; anabolic; neuroprotective; nephrotropic; ophthalmological; antilipsemic; dermatological, antiareresofleroic; antiarthritic; osteopathic; thrombolytic; nootropic; anorectic; hypotenaive; cytostatic; diabetic; ketosis; acidosis; diabetic neuropathy; diabetic nephropathy; diabetic nephropathy; bone disease; arthritis; bone disease; arteriosclerosis; thrombosis; hypotension; indigestion; memory loss; obesity; hypoglycemia; edema; insulin resistance; insulin allergy; fat metabolism disorder; cancer; mouse; murine; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and elcosanoid-binding G-protein coupled receptor protein, GPR40, originating in mouse, rat, crab-eating monkey and hamster (sequences fully defined in the specification), equivalent proteins of similar activity, and peptides containing partial sequences of the GPR40 protein. The novel fatty acid and GPR40 protein and their compositions have the following activities: antidiabetic, anabolic, neuroprotective, nephrotropic, ophthalmological, antilipaemic, dermatological, antiarthritic, osteopathic, thrombolyric, anotropic, antiarthritic, osteopathic, thrombolyric, and eicosanoid-binding G-protein coupled receptor protein, GPR40, and further compositions can be used in the treatment, prevention and diagnosis of diabetes, ketosis, acidosis, diabetic neuropathy, diabetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel screening method comprising a fatty and eicosanoid-binding G-protein coupled receptor protein, GPR40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patty acid and eicosanoid-binding G-protein coupled receptor protein GPR40 for control of pancreatic function and treatment of diabetes.
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Kawamata Y, Ogi K, Harada M, Fukusumi S;
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/partial
/note= "No stop codon"
/---Anct= "Mouse GPR40 protein"
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1. .900
/*tag= a
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                                                                                                                                                                              encoding mouse GPR40 protein.
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12-JUL-2002; 2002JP-00204163.
12-NOV-2002; 2002JP-00328696.
22-JAN-2003; 2003JP-00014032.
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                                                                                                   ADB61401 standard; DNA; 900
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nephropathy, diabetic retinopathy, hyperlipaemia, skin diseases, arthritis, bone diseases, arteriosclerosis, thrombosis, hypertension, indigestion, memory loss, obesity, hypoglycaemia, edema, insulin resistance, insulin allergy, fat metabolism disorders and cancer. This polymuclectide sequence represents the DNA encoding a mouse GPR40 protein of the invention.
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                                                                                                                                                                                                Sequence 900 BP; 137 A; 300 C; 244 G; 219 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                  Score 602.4; DB 9;
Pred. No. 1.1e-108;
0; Mismatches 186;
                                                                                                                                                                                                                                                    tch 66.7%;
al Similarity 79.3%;
714; Conservative
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and eicosanoid-binding G-protein coupled receptor protein, GPR40.

originating in mouse, rat, crab-eating monkey and hamster (sequences tully defined in the specification), equivalent proteins of similar activity, and peptides containing partial sequences of the GPR40 protein.

The novel fatty acid and GPR40 protein and their compositions have the following activities: antidiabetic, anabolic, neuroprotective, nephrotropic, optimal mological, antilipaemic, dermatological, antiartariosclerotic, antiarthritic, osteopathic, thrombolytic, notropic, anorectic, hypoteensive, and cytostatic. The novel fatty acid and elcosanoid-binding G-protein coupled receptor protein, GPR40, and closanoid-binding G-protein coupled receptor protein, GPR40, and elcosanoid-binding G-protein coupled receptor protein, GPR40, and elcosanoid-binding can be used in the treatment, prevention and diagnosis of diabetic retinopathy, diabetic neuropathy, diabetic retinopathy, hyposlipaemia, skin diseases, arteriosclerosis, thrombosis, hypertension, indigestion, memory loss, obesity, hyposlycaemia, edema, insulin insulin allergy, fat metabolism disorders and cancer. This polynucleotide sequence represents the DNA encoding a rat GPR40 protein of the invention.
                                                                                                                                                                                            fatty acid; eicosanoid-binding G-protein coupled receptor; GPR40; antidiabetic; anabolic; neuroprotective; nephrotropic; ophthalmological; antilipaemic; dermatological; antiarteritor; antiarteritic; osteopathic; thrombolytic; nocropic; anorectic; hypotenaive; cytostatic; diabetic; ketosis; acidosis; diabetic neuropathy; diabetic nephropathy; hyporlipaemia; skin disease; arthritis; bone disease; arteriosclerosis; thrombosis; hyportension; indigestion; memory loss; obesity; hypoglycemia; edema; insulin resistence; insulin allergy; fat metabolism disorder; cancer; rat; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fatty acid and eicosanoid-binding G-protein coupled receptor protein GPR40 for control of pancreatic function and treatment of diabetes.
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Kawamata Y, Ogi K, Harada M, Fukusumi S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "No stop codon"
/product= "Rat GPR40 protein"
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1. .900
                                     ADB61403 standard; DNA; 900 BP
                                                                                                                                                          encoding rat GPR40 protein
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12-NOV-2002; 2002JP-00328696.
22-JAN-2003; 2003JP-00014032.
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Kizawa H,
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                                                              Gaps
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                                     Length 900;
             Sequence 900 BP; 142 A; 287 C; 244 G; 227 T; 0 U; 0 Other;
                                  Score 588; DB 9; Length 90
Pred. No. 7.3e-106;
0; Mismatches 195; Indels
                                     65.1%;
                                   Query Match 65.1
Best Local Similarity 78.3
Matches 705; Conservative
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AAV53631 standard; cDNA; 1841 BP.

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Bergsma DJ, Sathe GM,
                                                           WPI; 1998-482962/42
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intracellular loop 3; transmembrane domain 6; drug screening; agonist;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    334 GTTCGTCTTCTCGGTGTACCTTCTCACTTTCCTGGTGGGGCTCCCCCTCAACCTGCTGCTGGC
                                                                                                                                                                                                      HNFDY20; G-protein coupled receptor; human; infection; HIV; pain; cancer; asthma; Parkinson's disease; acute heart failure; hypotension; hypertension; urinary retention; osteoporosis; angina pectoris; myocardial infarction; ulcer; allergy; benign prostatic hypertrophy; myocardial infarction; ulcer; allergy; benign prostatic hypertrophy; mental retardation; dyskinesia; manta depression; delirium; dementia; mental retardation; dyskinesia; Huntingdon's disease; ss. Gilles de la Tourette's syndrome; therapy; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTCTCCTTCGGCCTCTATGTGGCCGCCTTTGCGCTTGGGCTTCCCGCTCAACGTCCTGGC
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Pred. No. 4.7e-15;
0; Mismatches 326; Indels 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1841 BP; 334 A; 538 C; 593 G; 376 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mao JY;
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                                                                                                                          Human 7-transmembrane receptor HNFDY20 cDNA.
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125. 1330 /*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMIK ) SMITHKLINE BEECHAM CORP
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Best Local Similarity 52.3%;
Matches 383; Conservative (
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                                        (first entry)
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The invention relates to constitutively active, non-endogenous versions of endogenous human orphan G protein-coupled receptors (GPCRs, AAY96643-AAY90683-Y90687), and to DNA encoding them (AAA30708-A330743 and AAA30775-A30779). The mutant proteins of the invention contain a matation in a portion of the protein comprising intracellular loop 3 (CC) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X, is substituted for an endogenous residue in IC3 at a position 16 amino acids N-terminal of an endogenous proline in IC3 at a position 16 amino acids N-terminal of an endogenous proline in TM6 to form a sequence X-CC (AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg or Ala, and is preferably Lys. When the endogenous residue at this position is Lys, this residue is replaced by His, Arg or preferably Ala. The 15 amino acid stretch between the substituted amino acid and the Pro may be endogenous, non-endogenous, or a mixture of endogenous and non-endogenous credidues. The constitutively active GPCRs are useful for identifying antagonists and partial agonists for use as pharmaceutical captured are appeared by the receptors in normal and diseases and disorders associated with that receptor. Because the novel mutant GPCRs are constitutively active, they can be useful for treating diseases and disorders associated with that receptor. Because the novel mutant GPCRs are constitutively active, they can be used directly for screening of compounds without the need for endogenous ligands. The present sequence constitutively active, they can be used directly for screening of exemplification of the invention. This was cloned and subjected to site-directed mutagenesis (SDM) to generate DNA encoding the constitution of the invention. This was cloned and subjected to site-directed mutagenesis (SDM) to generate DNA encoding the constitution of the invention.
                                                                                                                                                                                                  Non-endogenous constitutively activated human G protein-coupled receptors, useful for identifying agonists for use as pharmaceutical
                                                                                                                                                                                                                                                                                                                  Example 1; Page 309-310; 341pp; English.
(AREN-) ARENA PHARM INC
                                                      Chalmers DT,
                                                                                                                WPI; 2000-329165/28.
P-PSDB; AAY90680.
                                                   Behan DP,
                                                                                                                                                                                                                                                               agents.
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24; Score 121.8; DB 3; Length 1041; Pred. No. 9.4e-15; 0; Mismatches 327; Indels 24; Sequence 1041 BP; 170 A; 324 C; 315 G; 232 T; 0 U; 0 Other; 13.5%; 52.1%; Best Local Similarity 52.1 Matches 382; Conservative Query Match

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137 197 344 105 ceregradaterregradecrecadedececeseseses and a consequence a conse 257 AGCCAATGGCATGCACTGGCCCTTCATCCTCTGCCCACTCTCTGGATTCATCTT 284 317 GGGAGCAGCCTTCCCCTTGGGCTACCAAGCCTTCCGGAGGCCGTGCTATTCCTGGGGGGT 377 404 Grececcentricescorregical and a second secon GTTCGTCTTCTCGGTGTACCTTCTCACTTTCCTGGTGGGGCTCCCCCTCAACCTGCTGGC 104 165 CAACCTGACCGCCTCGGACCTGCTCCTGCTGCTGTTCCTGCCTTTCCGCATGGTGGAGGC 224 GAGTGTGGCCTGCTGGCTTGGCCTCTGCTCACTGCAGCGTGGTCTACGTCATAGAATT 464 77 crircaccaccarciarcreaceeeercrirecreseaeerereaeearreaaeeerreer CATCCGAGGCGCGACGCCCACGCCCGGCTCCGTCTCACCCCTAGCCTGGTCTACGCCCT 138 GAACCTGGGCTGCTCCGACCTGCTGACAGTCTCTCTGCCCCTGAAGGCGGTGGAGGC GCTAGCCTCCGGGGCCTGGCCTCTGCCGGCCTTCTGCCCCGTCTTCGCGGTGGCCCCA CTICITCCCACTCIAIGCCGGCGGCGCTICCTGGCCGCCCTGAGTGCAGGCCGCTACCT GCTCTCCTTCGGCCTTATGTGGCCGCCTTTGCGCTTGGGCTTCCCGCTCAACGTCCTGGC Gaps 18 45 9. 225 318 198 285 258

563 740 506 557 617 620 680 TCCAGGAGGCTGGCTGGACCACAGCAACACCCTCCCTGGGCATCAACACACGGGTCAACGG 497 CCGGGCACTGGCCCGCCTCCGGCCTGACGCACAGGCGGAAGCTGCGGGCCGCCTGGGTGGC 617 ---acarcreceaeaeceaecaeeaeaeeae CTACCTGGAGTTCCGGAAGGACCAG--CTAGCCATCCTCCTGCCGTGCGGCTGGAG-AT CICICICCIGCICITITITICIGCCCTIGGCCATCACAGCCTTCTGCTACGTGGCTGCCT 564 gecigiogiccirciristegiccecrearcarcacaeciaciecrac---aeceeer CTCTCCGGTCTGCCTGGAGGCCTGGGACCCGGCCTCTGCCGGCCCGGCCCGGCTTCAGCCT 738 CAGCTTCCTGTAC 750 741 GGGCTATATCTGC 753 465 CTCAGGGG-618 507 558 498 원 ò 셤 ò 셤 ð 셤 8 g ઠે g

GPR 42; G-protein coupled receptor 42; human; drug screening; dyslipidaemia; coronary heart disease; atherosclerosis; thrombosis; obesity; angina; kidney failure; peripheral vascular disease; stroke; diabetes; metabolic syndrome; spadrome X; antilipaemic; cardiant; antiatherosclerotic; thrombolytic; anorectic; antianginal; nephrotropic; vasotropic; cerebroprotective; antidiabetic; gene therapy; ss. Human G-protein coupled receptor GPR 42 cDNA. AAH26460 standard; cDNA; 1041 BP (first entry) 29-OCT-2001 AAH26460; AAH26460

19-FEB-2001; 2001WO-GB000684. 18-FEB-2000; 2000GB-00003900. 22-MAR-2000; 2000GB-00007015. GLAX) GLAXO GROUP LTD 2001-536581/59 Wise A, Brown AJ; WO200161359-A2 23-AUG-2001.

Homo sapiens.

Identification of an agent for the modulation of G-protein coupled receptor useful for the treatment of disease i.e. dyslipidemia or stoke.

P-PSDB; AAB82759

Claim 16; Page 46-47; 53pp; English.

The present sequence is that of cDNA encoding human G-protein coupled receptor 42 (GPR 42, see AAB82759). The invention is based on the finding that expression of GPR 42 and GPR 41 (see AAB82758) is restricted to adipose tissue. GPR 41 or GPR 42 may therefore be used as a screening target for the identification and development of novel pharmaceutical agents for use in inhibiting lipolysis. Methods are claimed for identifying agents that modulate GPR 41 or GPR 42 activity, involving: (1) contacting a test agent with GPR 41 or GPR 42 or a variant capable of

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in the presence of a G-protein, thereby determining whether the test agent modulates activity. Such agents, which may be an activator of GPR 41 or GPR 42, an inhibitor of lipolysis, or a polymucleotide encoding GPR 41, GPR 42 or variant polypeptide, are useful for the treatment of dyslipidaemia, coronary heart disease, atherosclerosis, thrombosis or obesity, angina, chronic renal failure, peripheral vascular disease, stroke, type II diabetes or metabolic syndrome (syndrome X) (all claimed)
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coupling to a G-protein; and (2) monitoring for GPR 41 or GPR 42 activity
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Pred. No. 9.4e-15;
0; Mismatches 327; Indels 24;
                                                                                                                                                                                                                                                                                                                                    Sequence 1041 BP; 169 A; 321 C; 317 G; 234 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 52.1%;
Matches 382; Conservative
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Search completed: April 30, 2004, 15:41:49 Job time : 456 secs

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Title: Perfect :

Sequence:

nucleic

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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CA776599 1p08c01.y
CE038975 Ligr-gas-
AL270114 Tetracadon
BZ160914 CH230-339
AQ119988 1a2 3024 A
BZ160914 CH230-339
AQ119988 AGENCOURT
CD55955 AGENCOURT
CF147780 AGENCOURT
CF147780 AGENCOURT
CA777066 1p02f08.y
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BG190636 RST9710 A
AY403859 Mus muscu
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AX408184 Pan trogl
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AL059666 Drosophil
AL053013 Drosophil
AK049671 Mus muscu
AL194406 Terraodon
BM141985 if55b05.y
AZ409268 1M0180P17
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VIRTUAL TRANSCRIPT, partial sequence,
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AW138148 UI-H-BII-
AI344017 tc01e02.x
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 503)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Fodd,M.A., Tanembaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanembaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferritars, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 302 (5652), 1960-1963 (2003)
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CB730455
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CB038975
CNS041EX
AQ119988
BM544968
CP155955
CP157706
AQ119988
BM544968
CP157706
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AX408183
AX40861
AX05053663
CD559663
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AY411510.1 GI:39767478
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 AY411510 Homo sapi
AY411511 Pan trogl
AY411512 Mus muscu
AW583167 iallfil.y
                                                                                                          April 30, 2004, 14:33:11; Search time 2948 Seconds (without alignments) 9147.065 Million cell updates/sec
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               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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/gene="GPR40"
/locus_tag="HCM4248"
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Pan troglodytes
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Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
Location/Qualifiers
1. .903
//organism="Homo sapiens"
//organism="Homo sapiens"
//db xref="taxon:9606"
<1. .>903
//organism="Homo"
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Pred. No. 2.2e-148;
0; Mismatches 1; Indels 0;
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/locus_tag="HCM4248"
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Matches 902; Conservative
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Pan troglodytes GPR40 gene, VIRTUAL TRANSCRIPT, partial sequence, genemic survey sequence.
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Clark, A.G.; Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Reritera, S., Wanop, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Wite, T.J., Sninsky, J.J., Inferring nonneutral evolution from human-chimp-mouse orthologous
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This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
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/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"

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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Reritara, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M. P. Inferring nonneutral evolution from human-chimp-mouse orthologous
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This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
                                       TTCAGCCTCTCTCTCCTGCTCTTTTTTCTGCCCTTGGCCATCACAGCCTTCTGCTACGTG
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
<1. .>903
/gene="GPR40"
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tigr-gss-dog-17000315416692 Dog Library Canis familiaris genomic,
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The Institute for Genomic Research
Department of Enkaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
                        TCTGCGTAGGACCCTACAACGCCTCCAACGTGGCCAGCTTCCTGTACCCCAATCTAGGAG 763
                                                                                                                                               241 GCTCCTGGCGGAAGCTGGGGCTCATCACGGGTGCCTGGAGTGTGGTGGTCTTAATCCGCTGG 300
                                                                                                                                                                                                                                           61 CCGCTCAACGTCCTGGCCATCCGAGGCGCGACGGCCCACGCCCGGCTCCGTCTCACCCCT 120
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                                                                                                                                                                                                                  824 TGACCGGTTACTTGGGAAGGGGTCCTGGCCTGAAGACAGTGTGTGCGGCAAGAACGCAAG 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 Arggaccreccecededecrerrerredecererargredecereredeceredecerre
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1 (bases 1 to 522)
1 (kixness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.
                                                    181 TCTGCGTAGGACCCTACAACGCCTCCAACGTGGCCAGCTTCCTGTACCCCCAATCTAAGAG
                                                                                                                    1 ATGGACCTGCCCCGCAGCTCTCCTTCGGCCTCTATGTGGCCGCCTTTGCGCTGGGCTTC
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/note="Site_1: BstXI; Libraries were prepared from
peripheral blood"
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86.0%; Pred. No. 7.6e-44;
iive 0; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Canis familiaris"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/strain="Standard Poodle"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9615"
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                                                                                                                                                                                                                                                                                                                 884 GGGCAAGTCCCAGAAGTAA 903
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Fax: 301-838-0208
Email: ekirknes@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genomic survey sequence. CE730455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CE730455.1 GI:37070575
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Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 86.0
Matches 339; Conservative
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AUTHORS
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CE730455
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                                                                                                                    EST 13-MAR-2002
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Pax: 617-495-8557

Email: dmclton@blohp.harvard.edu
Libraries were constructed by Dr. Douglas Melton

DNA sequencing by: Washington University Genome Sequencing Center
For information on obtaining a clone please contact: Juliana Brown

This sequence now available from the IMAGE consortium, for clone orders contact: info@lmage.llnl.gov

Seq primer: -40RP from Gibco

High quality sequence stop: 421.
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( bases 1 to 443)

Melton, D., Meadows, A., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylle, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenae, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Human Pancreatic Islets"
/note=Torgan: Pancreas; Vector: pSPORT1; Site 1: Not 1;
Site_2: Sal 1; Library constructed using SuperScript
Plasmid Library kit (Life Technologies). cDNA made by
oligo-dr priming. Size-selected by column fractionation;
average insert size 1.08 kb. Primary library,
unamplified."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Endocrine Panoreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 TGGCCATCACAGCCTTCTGCTACGTGGGCTGCCTCCGGGCACTGGCCCACTCCGGCCTGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                  AW583167

443 bp mRNA linear EST 13-P
allfil.,14 Human Pancreatic Talete Homo sapiens CDNA clone
IMAGE:5638029 5' similar to SW:GP40 HUMAN 014842 PUTATIVE G
PROTEIN-COUPLED RECEPTOR GPR40. [1] ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washu-Harvard Pancreas EST Project
Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mkNa"
/db_xref="taxon:9606"
/clone="InAGRE:5638029"
/tiskue_type="Islets of Langerhans"
/dev stage="Adult"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .443
/organism="Homo sapiens"
                                                                                                                                                                                                                                      AW583167.1 GI:7260111
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                                                                                                                                                                                                                                                                                                                   Homo sapiens
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234 bp DNA linear GSS 24-SEP-2003 tigr-ges-dog-17000349748378 Dog Library Canis familiaris genomic, genoomic survey sequence.
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The Institute for Genomic Research
Department of Enkaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
                                                                                                                             322 CCGCTCAACGTCCTGGCCATCCGAGGCGCGAGGCCCCAGGCCCCGGCTCCGTCTCACCCCT 381
                                                                                                                                                                                                                                                                                               382 AGCCTGGTCTACGCCCTGAACCTGGGCTGCTCCGACCTGCTGACAGTCTCTCTGCCC 441
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Kirkness, E. P., Bafna, V., Halpern, A. L., Levy, S., Remington, K., Rusch, D. B., Delcher, A. L., Pop, M., Wang, W., Fraser, C. M. and Venter, J. C.
                                                                                                                                                                                                                                                                                                                                                                               442 CTGAAAGCGGGGAGGCGCTAAGCTCCGGAACTCTGCCAGACTCGCCTGCTCCCC
                                                                                                                                                                                       61 CCGCTCAACGTCCTGGCCATCCGAGGCGCGACGGCCCACGCCCCGGCTCCGGTCTCACCCCT
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/note="Site_l: BstXI; Libraries were prepared from
peripheral_blood"
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                     Score 295.2; DB 14; Length 609; Pred. No. 6.3e-42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 AGTGCAGGCCGCTACCTGGGAGCAGCCTTCCCCTTGGGCTACCAAGCC 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      562 AGCGAAGCCCGACCCCTGGTAGCCAGCCTAGGGCTACCAACCC 609
                                                              Indels
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                                                              33;
                                                              0; Mismatches
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/strain="Standard Poodle"
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1. .234
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Class: shotgun.
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CE038975.1 GI:35069198
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                     32.7%;
                     Query Match
Best Local Similarity 90.5
Matches 315; Conservative
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Fax: 301-838-0208
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                                                                             AGTGCAGGCCGCTACCTGGGAGCAGCCTTCCCCTTGGGCTACCAAGCCTTCCGGAGGCCG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 609)
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Cardenas, M., Theishin, B., Ritter, B., Ronko, I., Bennett, J., Williams, T., Jackson, Y. and Bowers, Y. Cole, R., Tasgarelshvili, R., Hilliams, T., Jackson, Y. and Bowers, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 617-495-1812

Pax: 617-495-8557

Ramail: dmelton@blohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Library was constructed by Dr. Hiroshi Inoue
Nashington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Seq primer: -40NP from Gibco
High quality sequence stop: 426.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
  CTGAAGGCGGTGGAGGCGCTTCCGGGGCCTGGCCTCTGCCGGCCTCGCTGTGCCCC
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Other ESTs: ip08c01.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
                                                                                                                                                                                                                                                                        361 TGCTATTCCTGGGGGGTGTGCGCGGCCATCTGGG 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CA776599.1 GI:26014474
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Homo sapiens
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181
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E 1 (bases 1 to 774)

S Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K.,
Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K.,
Shvattsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D.,
Riggs, F., de Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 MboI segment
Unpublished (1999)
Other GSSs: CH230-339G19.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CH230-339G19.TJ CHORI-230 Segment 2 Rattus norvegicus genomic clone BZ160914
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Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availablilty, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Regources
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  819 reaccarcecerrecerrecerracaacceracecracecerececerececrerere
                                                                                                                  137 TGAACCTGGGCTGCTCCGACCTGCTGACAGTCTCTCTGCCCCTGAAGGCGGGGAGG 196
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                                                                                                                                                                                                                                                                                                                                                            642 TCAACCTGTGCCTGGCCAACCTGGCCCTGGTGGCTTGGCTGCCCGTCAAGGCCCTGGAGA 701
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                       582 retregretacerecedaadederecaadedmodecededededederededededede
                                                          20 TCTCCTTCGGCCTCTATGTGGCCGCCTTTGCGCTTGGGGCTTCCCGGCTCAACGTCCTGGCCA
                                                                                                                                                                               80 TCCGAGGCGCCGACGCCCCG---GCTCCGTCTCACCCCTAGCCTGGTCTACGCCC
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3; Mismatches 159; Indels
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/mol type="genomic DNA"
/strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
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BZ160914
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This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more hiformation, please take a look at http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
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Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 074E14 of library G from Tetraodon nigroviridis, genomic survey
                                 234 CCCTGGGCATCAACACGCCGGTCAACGGCTCTCCAGTCTGCCTGGAGGCCTGGGAACCCTG
                                                                                                                     589
                                                                                                                                                174 CCTCAGGGGCCCCGCTCGCCTCTCTCTCCTGCTCTTCTTCCTGCCCCTGACCA 115
                                                                                                                                                                                                                                       590 TCACAGCCTTCTGCTACGTGGCTGCCTCCGGGCACTGGCCCCGGCTCAGGCCACA 649
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
CCCTGGGCATCAACACACACGGTCAACGGCTCTCCGGTCTGCCTGGAGGCCTGGGACCCGG 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Sautin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                         114 TCACGGCCTTCTGCTACGTGGGCTGCCTCCGGGCACTGGCCCCGCTCAGGCCACA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J. Estimate of human gene number provided by genome-wide analysis using Tetracdon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000)
                                                                                                                        CCTCTGCCGGCCCGGCTTCAGCCTCTCTCTCTCTGTCTTTTTTTCTGCCCTTGGCCA
                                                                                                                                                                                                                                                                                                                                                            650 GGCGGAAGCTGCGGGCCGCCTGGGTGGCCGGCGGGCCCTCCTCACGCTGCTG 702
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| Mmol Lype="qenomic DNA"
| Mmol Lype="qenomic DNA"
| Mmol Lype="texon:99883"
| Clone="074E14"
| Clone lib="G"
| More = "Genoscope sequence ID : COBG074BC07SP1~end
| PUC-Ori"
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                                                                                                                                                                                                                                                                                                                                                                                              54 GACGGAAGCTAAGGCCAGACTGGGGCCCGCCGGCGGCCTCTCTCACGCTGCTG
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Pred. No. 2.9e-13;
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AL270114.1 GI:7992019
GSS; genome survey sequence.
Tetracdon nigroviridis
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JOURNAL MEDLINE REFERENCE AUTHORS

TITLE

PUBMED

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ORIGIN

FEATURES

TITLE JOURNAL

COMMENT

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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

LOCUS DEFINITION

RESULT 8 CNS041EX

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Gaps

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/clone lib="NIH MGC_125"
/note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
/note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
stc_1: EcoRV (destroyed); Site_2: Not1; RNA source pool of three ovaries, from females ranging in age from 38 to 49 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 2:1 kb, insert size range 1-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BM544968
AGENCOURT_6497637 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5588752
                                                                                                                                                                                                                                                                             474 CCGCTCAACGTCCTGGCCATCCGAGGCGCGACGGNCCACGCNCGGCTCCGTCTCACCCCT 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12360 row: f column: 17
High quality sequence state: 26
High quality sequence state: 26
High quality sequence stop: 716.
                                                                                                                                                                                               414 AridaAccrecceccecaecrecerresecererargesecerrinesecerasecric 473
                                                                                                                                                                                                                                                61 CCGCTCAACGTCCTGGCCATCCGAGGCGCGACGGCCCACGCCCGGCTCCGTCTCACCCCT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 1117)

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                                                      Length 543;
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                                                                                                  Indels
                                                                                                                                                 1 ATGGACCTGCCCCCGCAGCTCTCCTTCGGCCTCTATGTGGCCGCCT
                                                 Score 128; DB 28;
Pred. No. 1.4e-12;
0; Mismatches 2;
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Matches 128; Conservative
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Best Local Similarity 52.1%;
Matches 371; Conservative
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Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQ119988 543 bp DNA linear GSS 22-SEP-1998 HS_3024_Al_H01_T7 CIT Approved Human Genomic Sperm Library D Homo Bapiens genomic clone Plate=3024 Col=1 Row=O, genomic survey
                                                                                                                                                                                                                                                                                                                                                61 CCGCTCAACGTCCTGGCCATCCGAGGCGCGACGCCCACGCCCGGCTCCGTCTCACCCCT 120
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/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
B-Coli DH108"
                  /sex="Pemale"
/cell_type="Brain"
/clone_lib="CHORI-230 Segment 2"
/note="Vector: pTARBACI.3; Site_1: MboI; Site_2: MboI;
CHORI-230 Rat (BN/SSNHSd/MCW) BAC library produced by
Pieter de Jong"
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                                                                                                                                                                                                                 Query Match
14.4%; Score 130; DB 28; Length 774;
Best Local Similarity 74.4%; Pred. No. 7.1e-13;
Matches 177; Conservative 0; Mismatches 60; Indels
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University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
T=1: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3024 row: O column: 1
Class: BAC ends
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db xref="teaxon:9606"
/clone="Plate=3024 Col=1 Row=O"
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Location/Qualifiers
/clone="CH230-339G19"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 779)
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National Institutes of Health, Mammalian Gene Collection
Unpublished (1999)
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/ilsue_type="mixed"
/ilsue_type="mixed"
/clone lib="NIH MGC 195"
/clone lib="NIH MGC 195"
/note="Vector: pDNR-Dual; Site_1: loxP-Sall; Site_2:
loxP-HindIII; Clones from this! library have been
PCR-amplified using gene-specific primers to contain the
PCR-amplified using gene-specific Primers for Rise DNA,
derived from with Refeeq. Template for PCR is EDNA,
derived from either pooled total RNA from 10 different tissues
(from BD Biosciences/Clontech and Mashington University).
PCR products are directionally cloned into the loxP sites
of the pDNR-Dual vector. Library constructed by Dr.
Narayan Bhat, Barl Bere III and Hongling Liao (Gene
Expression Laboratory, Research Technology Program, SAIC
Frederick, NGI-Frederick, Frederick, MD 21702). For
information on which gene each clone represents, please
visit our annownous fig site at
fip://image.llnl.gow/image/rearrayed_plates/IRBK.preSV.dat
a Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     138 GAACCTGGGCTGCTCCGACCTGCTGCTGACAGTCTCTCTGCCCCTGAAGGCGGTGGAGGC
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51.0%; Pred. No. 9.2e-09;
iive 0; Mismatches 309; Indels
Cound through the I.M.A.G.E. Consortium/LLNL
                                                   http://image.llnl.gov
Plate: IRBK1 row: e column: 10
High quality sequence stop: 748.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                      1. .779
/organism="Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:9606"
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Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
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                                                                                                                                                                           198 GCTAGCCTCCGGGGCCTGGCCGCCTCGGCTGTGCCCCGTCTTCGCGGTGGCCCA 257
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/db_xref="taxon:9913"
/tismue_type="pooled"
/lab_host="DH10B"
/clone_lib="WARC_IBOV"
/note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
Library made from pooled tissue from lymph node, ovary,
                                                                                                                                                                                                                                                                                                           CTTCTTCCCACTCTATGCCGGGGGGGTTCCTGGCCGCCCTGAGTGCAGGCCGCTACCT
                                                                                                          213 caaccitectriceaccitectricitectrecrecitectricitectriceceargesical
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ASS527 MARC 1BOV Bos taurus CDNA 5', mRNA sequence.
BIS41693
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USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Bos taurus"
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Seq primer: ATTTAGGTGACACTATAG.
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Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            438 TCCAGGAGGC 447
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Bos taurus
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/clone lib="NHH MGC 145"
/clone lib="NHH MGC 145"
/note="Vector: pcDNA3.1; Site 1: varies by clone; Site 2:
varies by clone; ORFs were PCR-amplified and cloned into pcDNA3.1 by the GPCR Consortium. Cloning sites vary by clone and include the following: 5'-EcoRv-KmnI/Khol-3', 5'-EcoRv-KmnI/Khol-3', EcoRv (TA cloned, non-directional). For information about which gene each clones represents, please visit our anonymous ftp site at ftp://image.lnl.gov/image/rearrayed_plates/IRBI.preSV.dat a Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST 25-JUL-2003
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Euthoria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 696)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-romail.nih.gov
Tissue Procurement: GPCR Consortium
CDNA Library Preparation: GPCR Consortium
CDNA Library Preparation: GPCR Consortium
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: WGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Plate: IRBI02 row: f column: 12
High quality sequence stop: 680.
                                                                                                   CCGGGCACTGGCCCCCCTCCCGCCTGACGCGGAAGCTGCGGGCCGCCTGGGTGGC
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National Institutes of Health, Mammalian Gene Collection (MGC)
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AGENCOURT_14740239 NIH_MGC_145 Homo sapiens cDNA clone IMAGE:6971953 5', mRNA sequence.
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/db_xref="taxon:9606"
/clone="IMAGB:6971953"
/tissue_type="mixed"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Schmitt, A., Theising, B., Ritter, E., Martin, J., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williama, T., Jackson, Y. and Bowers, Y. Cole, R., Tsagareishvili, R., Unpublished (2000)
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Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
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Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
                                                                                                                                                                                                                                                                                                          77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATCCGAGGCGCGACGGCCCACGCCCGGCTCCGTCTCACCCCTAGCCTGGTCTACGCCCT
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                                                                                                                              Length 472;
                                                                                                                          Query Match 11.4%; Score 102.8; DB 12; Length Best Local Similarity 53.8%; Pred. No. 3.7e-08; Matches 212; Conservative 0; Mismatches 182; Indels
Eat, hypothalamus, and pituitary."
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Seg primer: -40RP from Gibco
High quality sequence stop: 64.
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/clone lib="MRB5 islet"
//clone lib="MRB5 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
Not1; Site_2: Xho1; CDNA made by oligo-dr priming.
Size-selected on agarose gel. Average insert size -lkb. 5.
Xho1 site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."
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                                                                                                                                                                                                                                            /clone="IMAGE:6134918"
/tissue_type="Purified pancreatic islet"
/lab_host="DH108"
organism="Homo sapiens"
                                                                                     /mol_type="mRNA"
/db_xref="taxon:9606"
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Sequence 273, App
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Sequence 225, App
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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| Patent No. 5942416
| GENERAL INFORMATION:
| APPLICANT: Bergsma, Derk
| APPLICANT: Genesh, Sathe
| APPLICANT: Fuetterer, Wendy
| APPLICANT: Fuetterer, Wendy
| APPLICANT: Fuetterer; Wendy
| APPLICANT: Poetterer; Wendy
| APPLICANT: Poetterer; Wendy
| APPLICANT: Poetterer; Wendy
| APPLICANT: Fuetterer; Wendy
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SECOLD NO. 655339

GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Liaw, Chen W.

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GGGCTCATCACGGGGGCCTGGAGTGTGGTGTTAATCCGCTGGTGACCGGTTACTTGGGA
                                                                                                                     AACACAGGGCCAACAGGCTCTCCGGTCTGCCTGGAGGCCTGGGAGCCCCGGCCTCTGCCGGC
                                                                                                                                                                                                                                                                                                     COGGCCCGCTTCAGCCTCTCTCTCTCTTTTTCTGCCCTTGGCCATCACAGCCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGCTCATCACGGGTGCCTGGAGTGTGGTGCTTAATCCGCTGGTGACCGGTTACTTGGGA
                                                                                      GTCTTTGGGTTGGAGGCTCCAGGAGGCTGGACCACAGCAACACCTCCCTGGGCATC
                                                                                                                                                                                                                                                AACACACCGGTCAACGGCTCTCCGGTCTGCCTGGAGGCCTGGGACCCGGCCTCTGCCGGC
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Pred. No. 2.3e-176;
0; Mismatches 3;
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Best Local Similarity 99.7
Matches 900; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-170-496D-271
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US-09-170-496D-271
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677
                                                                                                                      910 geréregarcerceccagadesecacecaccéccéccadadadesececececerer 969
                                                                                                                                                                      678 CGGCGGGGCCCTCCTCACGCTGCTCTCTCGGTAGGACCCTACAACGCCTCCAACGTGGC 737
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                                                                         618 CCGGGCACTGGCCCGCTCCGGCCTGACGCACAGGCGGAAGCTGCGGGCCGCCTGGGTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: BERGSMA, DERK
APPLICANT: SATHE, GANESH M.
APPLICANT: PUETTEREK, WENDY
APPLICANT: MAO, JOYCE
TITLE OF INVENTION: CDNA CLONE HNFDY20 THAT ENCODES
TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPENATIOS SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/248,715
FILING DATE: 09-FEB-1999
CLASSIFICATION NUMBER: 08/820,521
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/820,521
FILING DATE: 19-MAR.1997
ATTONNEY/AGENT INFORMATION:
NAME: PRESETIA, PAUL P
REGISTRATION NUMBER: 23,031
REGISTRATION NUMBER: 23,031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GP-50011-1
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09248715
Patent No. 6207800
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: GF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0700
                                                                                                                                                                                                                                                                                                                    1030 GGÉCTATATCTGC 1042
                                                                                                                                                                                                                                                                      738 CAGCTTCCTGTAC 750
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Matches 383; Conservative
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CITY: Valley Forge
STATE: PA
COUNTRY: USA
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                                                                                     MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/820,521
FILING DATE: 19-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Han, William T 34,344
REGISTRATION NUMBER: 34,344
REPERENCE/DOCKET NUMBER: GH50011
TELECOMUNICATION INFORMATION:
TELEPRAK: 610-270-5219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1841 base pairs
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STRANDEDNESS: single
                                     ZIP: 19406
COMPUTER READABLE FORM
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                    COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.7%; Score 123.4; DB 3;
52.3%; Pred. No. 5.2e-17;
tive 0; Mismatches 326;
                                                                                                                                            NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GP-50011-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0700
                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-248-715-1
                                                             PRIOR APPLICATION DATA:
RAPLICATION NUMBER: 08/820,521
FILING DATE: 19-MAR-1997
ATTORNEY/AGENT INFORMATION:
                         FILING DATE: 09-Feb-1999
CLASSIFICATION: UNKNOWN
                                                                                                                                                                                                                                                                                                                                 LENGTH: 1841 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                        TELEX: 846169
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 13.7
Best Local Similarity 52.3
Matches 383; Conservative
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SATHE, GANESH M.
FUETTERER, WENDY
MAO, JOYCE
TITLE OF INVENTION: CDNA CLONE HNFDY20 THAT ENCODES
A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: Ratner & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA
COUNTRY: USA
ZIP: 19482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09248715
Patent No. 6277960
GENERAL INFORMATION:
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US-09-248-715-1
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393

Gaps

453 197 513 257 633 377 693 437 852 617 909

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APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
SEQ ID NO 273
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                                                                                         621 Gereregarceresecasas desecas de celeccio de desecas de desecas de construires de construires
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Pred. No. 4.8e-16;
0; Mismatches 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 273, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.1%;
51.8%;
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Best Local Similarity 51.8'
Matches 380; Conservative
                                                                                                                                                                                                                                                                                                                                             738 CAGCTTCCTGTAC
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CRGANISM: Homo sapiens
US-09-170-496D-273
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US-09-170-496D-273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREA
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT PILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
SEQ ID NO 253
970 GGGGCCACGCTGCTCCTTGTCTGCTTTGGGCCCTACAACGTGTCCCATGTCGT 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45 dricercircresisiacricrecatricensardesescreececrearecreeises 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105 CCTGGTGGTCTTCGTGGGCAAGCTGCAGCGCCCCCGGTGGCCCGTGGACGTGCTCCTGCT 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 13.5%; Score 121.8; DB 4; Length Best Local Similarity 52.1%; Pred. No. 1e-16; Matches 382; Conservative 0; Mismatches 327; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 GCTCTCCTTCGGCCTCTATGTGGCCGCCTTTGCGCTGGGCTTCCCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 253, Application US/09170496D Patent No. 6555339 GENERAL INFORMATION:
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US-09-170-496D-253
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US-09-170-496D-253
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; Patent No. 6436400
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Evenell, Scott R.
APPLICANT: Presentl, Scott R.
APPLICANT: Presentl, Scott R.
TITLE OF INVENTION: PRAF4 (ZCHEMR2)
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STRETT: 1201 Eastlake Avenue East
CITY: Scattle
STATE: WA
COUNTRY: USA
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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9.4%; Score 84.6; DB 3;
Best Local Similarity 47.2%; Pred. No. 5.4e-09;
Matches 329; Conservative 0; Mismatches 359;
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEE for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/053,866
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STRET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
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ATTORNEY/AGENT INFORMATION:
NAME: Leith, Debra K
REGISTRATION NUMBER: 32,619
REFERENCE/POCKET NUMBER: 98-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Coding Sequence
LOCATION: 176...1330
OTHER INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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9.4%; Score 84.6; DB 4; Length 4
Best Local Similarity 47.2%; Pred. No. 5.4e-09;
Matches 329; Conservative 0; Mismatches 359; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09472130A
; Patent No. 6473765
; GENERAL INFORMATION:
; APPLICANT: Xu, Wenfeng
; APPLICANT: Yee, David P.
; APPLICANT: Yee, David P.
; APPLICANT: Foster, Donald C.
; TITLE OF INVENTION: PROTEASE-ACTIVATED RECEPTOR PAR4
; TITLE OF INVENTION: (ZCHEMR2)
; TITLE OF INVENTION: (ZCHEMR2)
; TITLE OF INVENTION: QCOO-01-07
; TITLE REFERENCE: 98-10D2
; CURRENT APPLICATION NUMBER: US/09/472,130A
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/053,866
; RING RILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 21
; SEQ ID NOS: 21
; SEQ ID NOS: 21
; SEQ ID NOS: 21
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; LOCATION: (176)...(1330)
US-09-472-130A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCTGGGGGGTGTGCGCCGCCATCTGGGCCCTCGTCCTGTGTCACCTGGGTCTGGTCTTTG 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      753 cccrriciaericriciaridericerricia - - crearidecescescerescarriceceria 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       810 CACTGCAGCGGCAGACCTTCCGGCTGGCGCGCTCCGATCGCGGTGCTCTGCCATGACGCGC 869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               488 CGGTCAACGGCTCTCCGGTCTGCCTGGAGGCCTGGGACCCGGCCTCTGCCGGCCCCGGCCC 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             derrentrichedechedecharechedrarechaededeckeerechedaederred 989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGTTGGAGGCTCCAGGAGGCTGGCTGGACCACAGCAACACCTCCCTGGGCATCAACACACA 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  459 ATGGGCTGGCGCTGTGGGTGCTGGCCACGCAGGCACCTCGGCTGCCCTCCACCATGCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          633 CGGCCGCACTCTATGGTCACATGTATGGCTCAGTGCTGCTGCTGGCCGCCGCCGTCAGCCTGG
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/479,130
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                   PILING DATE:
ATYONEY/AGENT INFORMATION:
NAME: Leith, Debra K
REGISTRATION NUMBER: 32,619
REFERENCE/DOCKET NUMBER: 98-10
TELECOMUNICATION INFORMATION:
TELEFHONE: 206-442-6674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Coding Sequence
LOCATION: 176...1330
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 4895 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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APPLICANT: Behan, Dominic P.
APPLICANT: Halmers, Derek T.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-CTITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
SEQ ID NO 225
ILENGTH: 1098
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APPLICANT: Derk J. Bergsma, Catherine E. Ellis
APPLICANT: Derk J. Bergsma, Catherine E. Ellis
TITLE OF INVENTION: A No. 5912335el G-Protein Coupled Receptor
TITLE OF INVENTION: HUVCT36
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road, P.O. Box 1539
CITY: King of Prussia
STATE: PA
COUNTRY: USA
COUNTRY: USA
TITLE 19406-0939
COUNTRY: USA
TITLE 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MD STORAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.9%; Score 80; DB 4; Length 1098; 11.8%; Pred. No. 4.2e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM 486
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
SOFTWARE: WORDERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,974A
FILING DATE: October 3, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08724974A Patent No. 5912335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51.8%;
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Matches 207; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Homo
US-09-170-496D-225
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US-08-724-974A-1
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APPLICANT: Behan, Dominic P.

APPLICANT: Chalmers, Derek T.

APPLICANT: Liaw, Chen W.

TITLE OF INVENTION: Receptors

TITLE OF INVENTION: Receptors

FILE OF INVENTION: Receptors

FILE OF INVENTION: Receptors

TITLE OF INVENTION: 1998-10-13

WUMBER OF SEQ ID NOS: 294

SOFTWARE: Patentin version 3.1

SEQ ID NO 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             306 AGGCCGCTACCTGGGAGCAGCCTTCCCCTTGGGCTACCAAGCCTTCCGGAGGCCGTGCTA 365
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Pred. No. 4.2e-08;
0; Mismatches 190; Indels
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US-09-170-496D-225
S. Sequence 225, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 117, Application US/09170496D Patent No. 6555339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 51.8%;
Matches 207; Conservative
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US-09-170-496D-117
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US-09-170-496D-117
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377 CATCCACCAGACGCTGGCCCCGGTGGTCTATGTTACCGTGCTGGTGGTGGCGTTCCCGGC 436
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                                                                                                                                                                                                                                                                                                                                              Length 1697;
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Best Local Similarity 51.8%; Pred. No. 4.3e-08;
Matches 207; Conservative 0; Mismatches 190; Indels
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Patent No. 6645726
GRNERAL INFORMATION:
APPLICANT: Howard, Andrew D.
APPLICANT: Palyth, Oksana C.
APPLICANT: Smith, Roy G.
APPLICANT: Tan, Carina P.
TITLE OF INVENTION: CANINE GROWTH HORMONE SECRETAGOGUE
TITLE OF INVENTION: RECEPTOR
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CURRENT FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: PCT/US99/17915
PRIOR FILING DATE: 1999-08-06
PRIOR FILING DATE: 1998-08-06
PRIOR FILING DATE: 1998-08-10
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FASISEQ for Windows Version 4.0
SEQ ID NO 1
         PRIOR FILING DATE: 1998-12-04
PRIOR APPLICATION WUMBER: 60/121,851
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin version 3.1
SEQ ID NO 26
LENGTH: 1697
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NAME/KEY: misc_feature

LOCATION: (1)...(1050)

OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                                                    TYPE: DNA
CRGANISM: Homo sapiens
US-09-364-425B-26
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US-09-762-661A-1
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APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
APPLICANT: Lia, I-Lia
APPLICANT: Liam, I-Lia
APPLICANT: Lowitz, Kevin P.
APPLICANT: Chen, Ruoping
TILE OF INVENTION: Endogenous, Constitutively Activated G Protein-Coupled Orphan Rece
FILE REPERENCE: Aren0047
CURRENT APPLICATION NUMBER: 60/094, 879
FRICH APPLICATION NUMBER: 60/094, 879
FRICH FILING DATE: 1998-10-30
FRICH FILING DATE: 1998-10-30
FRICH FILING DATE: 1998-10-30
FRICH FILING DATE: 1998-10-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.9%; Score 80;
51.8%; Pred. No.
CLASSIPICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: William T. Han
REGISTRATION NUMBER: 34,344
REPERENCE/DOCKET NUMBER: 34,344
REPERENCE/DOCKET NUMBER: ATGS0022
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270 5094
TELEFRX: 610 270 5090
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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; Sequence 26, Application US/09364425B
; Patent No. 6653086
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1597
TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: Linear ANTI-SENSE: No
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us-10-202-687-1.rni

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                                                                                                               Gaps
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     Length 1050;
Query Match 8.7%; Score 78.2; DB 4; Length 1 Best Local Similarity 47.9%; Pred. No. 9.7e-08; Matches 292; Conservative 0; Mismatches 309; Indels
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Search completed: April 30, 2004, 15:43:30 Job time : 93 secs

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April 30, 2004, 15:43:35 ; Search time 465 Seconds (without alignments) 8784.275 Million cell updates/sec
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| cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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| cgn2_6/ptodata/1/pubpna/US07_NBW PUB.seq:*
| cgn2_6/ptodata/1/pubpna/PCTUZ_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/PCTUZ_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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| cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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	Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
	ΙD	US-10-251-385-249	US-10-225-567A-474	US-10-029-386-22904	US-10-202-687-1	US-10-251-385-271	US-10-029-386-9201	US-10-029-386-24088	US-10-251-385-253	US-10-225-567A-604	US-10-203-539-1	US-10-203-539-3	US-10-029-386-25146	US-10-251-385-273	US-10-225-567A-515
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121 AGCCTGGTCTACGCCCTGAACCTGGGCTGCTCCGACCTGCTGCTGACAGTCTCTCTGCCC 180

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ALIGNMENTS

Sequence 249, Application US/10251385
; Publication No. US20030105292A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Law, Chen W.
; TITLE OF INVENTION: Protein-Coupled
; TITLE OF INVENTION: Protein-Coupled
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT FILING DATE: 2002-09-20
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SEQ ID NO 249
; SEQ ID NO 249
; SEQ ID NO 249 ö မ 1 ATGGACCTGCCCCCGCAGCTCTCCGCCCTCTATGTGGCCGCCTTTGCGCTGGGCTTC Gaps ö Length 903; Indels Query Match
100.0%; Score 903; DB 15;
Best Local Similarity 100.0%; Pred. No. 3.8e-210;
Matches 903; Conservative 0; Mismatches 0; TYPE: DNA ORGANISM: Homo sapiens RESULT 1 US-10-251-385-249 US-10-251-385-249

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100.0%; Pred. No. 3.8e-210;
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; LENGTH: 903
; TYPE: DNA
; ORGANISM: HOMO 8:
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US-10-225-567A-474

i Sequence 474, Application US/10225567A

j Publication No. US20030113798A1

j GENERAL INFORMATION:
   APPLICANT: LifeSpan Biosciences
   APPLICANT: Brown, Joseph P.
   APPLICANT: Burmer, Glenna C.
   APPLICANT: Roush, Christine L.
   TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
   TITLE OF INVENTION: ANTIGENIC PEPTIDES.
   CURRENT FILING DATE: 2001-12-19
   PRIOR APPLICATION NUMBER: 60/257,144
   PRIOR PILING DATE: 2000-12-19
   NUMBER OF SEQ ID NOS: 2292

NUMBER OF SEQ ID NOS: 2292
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CTGAAGGCGGTGGAGGCGCTAGCCTCCGGGGCCTTGGCCTCTGCCGGCTCGTGTGCCCC
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Sequence 1, Application US/10202687

Publication No. US20040019109A1

GENERAL INFORMATION:
APPLICANT: OWNAN, CHRISTER
APPLICANT: OLDE, BJORN
APPLICANT: NILSSON, NICLAS
APPLICANT: FLODGREN, ERIX
TITLE OF INVENTION: METRADES OF IDENTIFYING COMPOUNDS AFFECTING FATTY ACID
TITLE OF INVENTION: METRADES US/10/202,687
CURRENT APPLICATION NUMBER: US/10/202,687
CURRENT FILING DATE: 2002-07-24
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
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ORGANISM: Homo sapiens
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Matches 903; Conserv
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                                    Sequence 22904, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David K.
ATILLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT PILLING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 22904
LENGTH: 903
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                                                                                                                                                                                                                                                                                                                       TYPE: DNA

ORGANISM: Homo sapiens

FRATURE:
OTHER INFORMATION: MAP TO U62631.1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.89
OTHER INFORMATION: WILL HIT: 9111526668, EVALUE 0.00e+00
OTHER INFORMATION: SWISSPROT HIT: 014842, EVALUE 0.00e+00
OTHER INFORMATION: EST_HUMAN HIT: AWS83167.1, EVALUE 0.00e+00
US-10-029-386-22904
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100.0%; Pred. No. 3.8e-210;
tive 0; Mismatches 0;
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                                US-10-029-386-22904
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QY 1 ATGGACCTGCCCCGCAGCTCTCCTTCGGCCTCTATGTGGCCTTTGCGCTGGGCTTC 60 Db 1 ATGGACCTGCCCCGCAGCTCTCCTTCGGCCTCTATGTGGCCGCTTTGCGCTTGGGCTTC 60	Qy 61 COGCTCAACGTCCTGGCCATCCGAGGCGCGAGCCCAACGCCCGGCTCCGTCTCACCCT 120 bb 61 CCGCTCAACGTCCTGGCCATCCGAGGCGCGAGGCCCAACGCCGGGCTCCGTCTCACCCT 120	Qy 121 AGCCTGGTCTACGCCCTGAACCTGGGCTGCTCCGACCTGCTGCTGCTGCTCTCTGCCC 180 121 AGCCTGGTCTAACCCTGAACCTGGGCTGCTCCGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	Oy 181 CTGAAGGCGTGGAGGCGTAGCCTCCGGGGCCTTGCCGGCTCGCTGTGCCCC 240	Oy 241 GICITGGGGTGGCCCACTICTICCCACTCTATGCCGGGGGGCTTCCTGGCCGCCTG 300 [Qy 301 AGTGCAGGCCGCTACCTGGGAGCCTTCCCCTTGGGCTACCAAGCCTTCCGGAGGCCG 360	Oy 361 IGCTATTCCTGGGGGGTGTGCGCGCCATCTGGGCCCTCGTGTGACCTGGGTCTG 420	Qy 421 GTCTTTGGGTTGGAGGCTCGGAGCAGCAGCAACACCTCCTGGGCATC 480 LILILIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	QY 481 AACACAGGTCAACGGCTCTGCGGTGCCTGGGACCCGGCCTCTGCCGGC 540 B 1	Qy 541 CCGGCCCGCTTCAGCCTCTCTCTCTCTTTTTTCTGCCCTTGCCATCACAGCCTTC 600	QY 601 TGCTACGTGGGCTGCCTCCGGGCACTGGCCCGGCTCCGGCCACAGGGGAAGCTG 660	Oy 661 CGGGCCGCCTGGGGGGGGGGCCCTCCTCACGCTGCTGCTGCGTAGGACCCTAC 720	OY 721 AACGCCTCCAACGTGGCCAGCTTCCTGTACCCCAATCTAGGAGGCTCCTGGGGGAAGCTG 780	QY 781 GGGCTCATCACGGGTGCCTGGAGTGTGGTGCTTAATCCGCTGGTGACCGGTTACTTGGGA 840 Db 781 GGGCTCATCACGGGTGCCTGGAGTGTGTGTTAATCCGCTGGTGACCGGTTACTTGGGA 840	QY 841 AGGGGTCCTGGCCTGAAGACAGTGTGTGCGGCAAGACGCAAGGGGGGCAAGTCCCAGAAG 900 DD 841 AGGGTCCTGGCCTGAAGACAGTGTGTGTGCGCAAGAACGCAAGGGGGCAAGTCCCAGAAG 900	Qy 901 TAA 903	Db 901 TAA 903	RESULT 6 US-10-029-386-9201 ; Sequence 9201, Application US/10029386	<pre>; Publication No. US20030194704A1 ; GENERAL INFORMATION: ; APPLICANT: Penn, Sharron G. ; APPLICANT: Rank, David R. ; APPLICANT: Hanzel, David K.</pre>
Ay 301 AGTGCAGGCGCTACCTGGGAGCAGCCTTCCCCTTGGGCTACCAAGCCTTCCGGAGGCCG 360	dy 361 TGCTATTCCTGGGGGGTGTGCGCGGCCATCTGGCCCTCGTCTGTGTCACCTGGGTCTG 420 bb 361 TGCTATTCCTGGGGGGGGCGATCTGGGCCCTCGTCTCTGTGTCACCTGGGTCTG 420	dy 421 GTCTTTGGGTTGGAGGCTCCAGGAGGCTGGTGGACCACACACCTCCCTGGGCATC 480 Db 421 GTCTTTGGGTTGGAGGCTCCAGGAGGTTGGTCTGGTTGGT	Qy 481 AACACACCGGTCAACGGCTCTCCGGTCTGCTGGAGCCTGGGACCCGGCCTTGCCGGC 540 Db 481 AACACACCGGTCAACGGTCTCCGGTCTGCTGGAGGCCTGGGAGCCTGGCGGC 540	QY 541 CGGGCCGCTTCAGCCTCTCTCTCTCTTTTTTTTGGCCTTGGCCATCACGCTTC 600 Db 541 CGGCCCGCTTCAGCCTCTCTCTCTCTCTTTTTTTTTTGGCCATCACACCTTC 600	Oy 601 TGCTACGTGGCTGCCTCCGGCCACTGGCCTCCGGCCTGACGCACGGGGAAGCTG 600 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy 661 CGGGCCGCTCGGGTGGCCGGGGGGCCCTCCTCACGGTGCTGCTGCGTAGGACCCTAC 720 Db 661 CGGGCCGCTGGGTGGCGGGGGCCCTCCTCACGTGCTGCTGCTAGGACCCTAC 720	Qy 721 AACGCCTCCAACGTGCCCAGCTTCCTGTACCCCAATCTAGGAGGCTCCTGGCGGAAGCTG 780 Db 721 AACGCCTCCAACGTGGCCAGCTTCCTGTACCCCAATCTAGGAGGCTCCTGGCGGAAGCTG 780	Qy 781 GGGCTCATCACGGGGTGCCTGAGGTGTGCTTAATCCGCTGGTGACCGGTTACTTGGGA 840 Db 781 GGGCTCATCACGGGTGCTGGGTGCTTAATCCGCTGGTGACCGGTTACTTGGGA 840	QY 841 AGGGTCCTGGCCTGAAGACAGTGTGCGGCAAGAAGGGGGGCAAGTCCCAGAAG 900	CY 901 TAA 903 Db 901 TAA 903	RESULT 5 US-10-251-385-271 • Seminance 271, Annlication US/10251385	Publication No. US20030105292A1; GENERAL INFORMATION: APPLICANT: Behan, Dominic P.	<pre> ; APPLICANT: Chalmers, Derek T. ; APPLICANT: Liaw, Chen W. ; TITLE OF INVENTION: No. US20010105292Al-Endogenous, Constitutively Activated Human G ; TITLE OF INVENTION: Protein-Coupled ; TITLE OF INVENTION: Protein-Coupled</pre>	; TITLE OF INVENTION: Receptors ; FILE REFERENCE: AREN-0040 ; CURRENT APPLICATION NUMBER: US/10/251,385 ; CURRENT FILING DATE: 2002-09-20	; PRIOR APPLICATION NUMBER: US/09/170,496 ; PRIOR PILING DATE: 1998-10-13	Normers Co Set 10 NOS: 231 SOFTWARE: Patentin version 3.1 SOFTWARE: Patentin version 3.1	7 TYPE IN 303 7 TYPE IN 4 7 ORGANISM: Homo sapiens US-10-251-385-271	Query Match 99.5%; Score 898.2; DB 15; Length 903; Best Local Similarity 99.7%; Pred. No. 5.6e-209; Matches 900; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Sequence 253, Application US/10251385

Publication No. US20030105292A1

GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
TITLE OF INVENTION: Receptors
TITLE OF INVENTION: Receptors
TITLE OF INVENTION: Receptors
TITLE OF INVENTION: 102/20030105292A1-Endogenous, Constitutively Activated Human G
TITLE OF INVENTION: 2002-09-20
TITLE OF INVENTION: 2002-09-20
CURRENT APPLICATION NUMBER: US/10/251,385
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
SEQ ID NO 253
LENGTH: 1041
TYPE: DNA
TYPE: DNA
CREANTSM: Homo sapiens
US-10-251-385-253
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO FILE REFERENCE: AEOMICA-X-2 CURRENT APPLICATION NUMBER: US/10/029,386 CURRENT PILING DATE: 2001-12-20 NUMBER OF SEQ ID NOS: 34288 SOFTWARE: Annomax Sequence Listing Engine vers. 1.1 SEQ ID NO 9201
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                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: MAP TO U62631.1

OTHER INFORMATION: EXPRESEED IN HELA, SIGNAL = 1.1

OTHER INFORMATION: EXPRESEED IN BONE MARROW, SIGNAL = 0.89

OTHER INFORMATION: SWISSPROT HIT: 014842, EVALUE 1.006-22

OTHER INFORMATION: EST HUMAN HIT: AU117321.1, BYALUE 2.006-01

OTHER INFORMATION: NT HIT: U62631.1, EVALUE 0.006+00
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EXPRESSED IN HELA, SIGNAL = 2.7

EXPRESSED IN BRAIN, SIGNAL = 1.7

EXPRESSED IN HEARY, SIGNAL = 1.5

EXPRESSED IN HEARY, SIGNAL = 1.5

SWISSPROT HIT: 015229, EVALUE 0.00e+00

NT HIT: AF024689.1, EVALUE 0.00e+00

EST_HUMAN HIT: AA860692.1, EVALUE 2.20e-02
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Pred. No. 2.5e-20;
0; Mismatches 327; Indels
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hankel, David R.
TITLE OP INVENTION: EXPRESSION ANALYSIS TWO
TITLE OP INVENTION: EXPRESSION ANALYSIS TWO
TITLE OP INVENTION: EXPRESSION ANALYSIS TWO
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT APPLICATION NUMBER: US/10/029,386
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 24088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.1%; Score 154; DB 15; 100.0%; Pred. No. 3.9e-28;
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US-10-029-386-24088
Sequence 24089, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
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Best Local Similarity 52.1
Matches 382; Conservative
                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
PEATURE:
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ORGANISM: Homo sapiens
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INFORMATION:
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Publication No. US20030113810A1
GENERAL INFORMATION:
APPLICANT: GLAXO GROUP LIMITED
TITLE OF INVENTION: NOVEL ASSAY
FILE REFERENCE: PG3849USw
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52.1%;
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APPLICANT: Burmer, Glenna C.
APPLICANT: Burmer, Clenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT PILLING DATE: 2000-12-19
PRIOR FILLING DATE: 2000-12-19
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Pred. No. 2.5e-20;
0; Mismatches 327; Indels
CURRENT APPLICATION NUMBER: US/10/203,539;
CURRENT FILING DATE: 2002-08-09;
PRIOR APPLICATION NUMBER: GB 0003900.8
PRIOR FILING DATE: 2000-02-18
PRIOR PILING DATE: 2000-03-12;
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 3.0
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Pred. No. 2.5e-20;
0; Mismatches 327; Indels 24;
RESULT 11
US-10-203-539-3
Sequence 3, Application US/10203539
Sequence 3, Application US/10203539
Publication No. US20030113810A1
GENERAL INFORMATION:
APPLICANT GLAXO GROUP LIMITED
TITLE OF INVENTION: NOVEL ASSAY
FILE REFERENCE: PG3849USW
CURRENT APPLICATION NUMBER: US/10/203,539
CURRENT FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: GB 0003900.8
FRIOR FILING DATE: 2000-03-18
FRIOR FILING DATE: 2000-03-18
FRIOR FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 3.0
SOFTWARE: Patentin Ver. 3.0
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13.5%;
Best Local Similarity 52.1%;
Matches 382; Conservative
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; LOCATION: (1)..(1041)
US-10-203-539-3
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Substitution US/10251385

Publication No. US20030105292A1

GENERAL INFORMATION:
GENERAL INFORMATION:
JAPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
TITLE OF INVENTION: No. US20030105292A1-Endogenous, Constitutively Activated Human G.
TITLE OF INVENTION: Receptors
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: US/09/170,496
PRIOR PAPLICATION NUMBER: US/09/170,496
PRIOR PLING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
SEQ ID NO 273
LENGTH: 1041
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                                                                672 CTACCTGGAGTTCCGGAAGGACCAG--CTAGCCATCCTCCTGCCCGTGCGGCTGGAG-AT
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Pred. No. 1.5e-19;
0; Mismatches 329; Indels
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Best Local Similarity 51.8
Matches 380; Conservative
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Publication No. US20030194704A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Barid K.
ATILLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT PILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 25146
LENGTH: 1206
                                                                                                    740
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                                    CGGCGGGGCCCTCCTCACGCTGCTGCTCTGCGTAGGACCCTACAACGCCTCCAACGTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTHER INFORMATION: MAP TO U62631.1
CTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.4
OTHER INFORMATION: EXT HUMAN HIT: BF115946.1, EVALUE 2.80e-02
OTHER INFORMATION: SWISSPROT HIT: 014843, EVALUE 0.00e+00
OTHER INFORMATION: NT HIT: U62631.1, EVALUE 0.00e+00
US-10-029-386-25146
                                                                                                                                                                         738 CAGCTTCCTGTAC 750
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US-10-029-386-25146
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Preshall, SCOLT R.
Yee, David P.
FOSTET, DONAIG C.
FITLE OF INVENTION: PROTEASE-ACTIVATED RECEPTOR
PAR4 (ZCHEMR2)
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OPERATING SYSTEM: DOS
SOFTWARE: PastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/187,049
FILING DATE: 28-Jun-2002
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  668 CCTGGGTGGCCGGGGGCCCTCCTCACGCTGCTGCT
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ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: «Unknown»
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Leith, Debra K
REGISTRATION NUMBER: 32,619
REFERENCE/DOCKET NUMBER: 98-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
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Publication No. US20030143218A1
GENERAL INFORMATION:
APPLICANT: Xu, Wenfeng
Presnell, Scott R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 206-442-6674
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ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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SEQUENCE CHARACTERISTICS:
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STATE: WA
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Publication No. US20030113798A1
EMBERGAL INFORMATION:
APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
APPLICANT: AND MATISENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS FILE REFERENCE: 1920-4-4
CURRENT PAPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
RIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                    557
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Pred. No. 2.4e-11;
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US-10-225-567A-515
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9.4%; Score 84.6; DB 15; Length 4895;
Best Local Similarity 47.2%; Pred. No. 2.4e-11;
Matches 329; Conservative 0; Mismatches 359; Indels 9;
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                                                  Search completed: April 30, 2004, 18:51:27 Job time : 468 secs
LENGTH: 4895 base pairs
                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

April 29, 2004, 12:03:33 ; Search time 59 Seconds (without alignments) 1436.682 Million cell updates/sec

US-10-202-687-2 1584

Title: Perfect score:

1 MDLPPQLSFGLYVAAFALGF.....RGPGLKTVCAARTQGGKSQK 300 Scoring table: Sequence:

1586107 segs, 282547505 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq 29Jan04:*

1: geneseqp1980s:*
2: geneseqp2090s:*
3: geneseqp2001s:*
5: geneseqp201s:*
6: geneseqp203s:*
7: geneseqp203bs:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

SUMMARIES

																				•					
tion	9 Human G p	6 Human G p	Human	4 Human GPR	9 Human G p	_	1 Human G p	6 Monkey GP	7 Mouse G p	0 Mouse GPR	2 Rat GPR40	8 Hamster G	9 Human G-p	Human	B Human G-p	5 Human G p	3 Human G p	4 Human 7-t	5 Human mut	3 Human G p	3 Mouse GCR	9 Mouse 7-t	4 Human GCR	Human	1 Human G p.
Description	Aay90679	Abg3110	Abp81994	Adb61404	Adc2276	Aay90684	Adc2279	Adb61416	Abg31107	Adb6140	Adb61402	Adb61428	Aab82759	Aay90680	Aab82758	Abp81715	Adc2277	Aaw59924	. Aay90685	Adc22793	Aay05383	Aay94269	Aay05384	Aaw59906	Aay90681
SUMMAKIES	AAY90679	ABG31106	ABP81994	ADB61404	ADC22769	AAY90684	ADC22791	ADB61416	ABG31107	ADB61400	ADB61402	ADB61428	AAB82759	AAY90680	AAB82758	ABP81715	ADC22773	AAW59924	AAY90685	ADC22793	AAY05383	AAY94269	AAY05384	AAW59906	AAY90681
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Length	300	300	300	300	300	300	300	300	300	300	300	300	346	346	346	346	346	401	346	346	330	330	330	330	330
% Query Match	100.0	100.0	100.0	100.0	100.0	7.66	7.66	95.9	84.2	84.2	83.3	81.8	23.1	21.9	21.9	21.9	21.9	21.9	21.6	21.6	21.5	21.5	21.1	21.0	21.0
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Result No.	н	7	m	4	ហ	9	7	ω	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Abp81990 Human G p Abr82313 Human G-p Adv22777 Human G-p Adv22775 Human G p Adv75058 Human mut Adc22795 Human G p Aaw75245 Fragment Aae271149 Human gen Aae27149 Human gen Abb65022 Human gen Abb82760 Rat G-pro Abg73510 X. laevie Abg73510 X. laevie Aay79597 Guinea pi Aay50135 Human pro Aay50135 Human pro	Aay50138 Mutant hu Aay15082 Human pro Aay45036 Human pro Aab47623 Human PAR Aag79604 Human PAR Abg73512 Human PAR
ABP81990 ABR82313 ADC22777 AAY90686 ADC22795 AAW75245 AAW77011 AAE27011 AAE27010 ABG73510 AAG73597 AAK70135 AAK50135	AAYS0138 AAY15082 AAY45036 AAB47623 AAG79604 ABG73512
3330 6 8 3330 6 8 3330 8 9 3330 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	2 5 5 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5
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0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	44 44 44 44 44 44 44 44 44 44 44 44 44

ALIGNMENTS

G protein-coupled receptor; GPCR; constitutively active; intracellular loop 3; transmembrane domain 6; drug screening; agonist; Human G protein-coupled receptor GPR40. AAY90679 standard; protein; 300 AA. Liaw CW; 98US-00170496. 99WO-US023938. (first entry) Chalmers DT, (AREN-) ARENA PHARM INC WPI; 2000-329165/28. WO200022129-A1. 13-OCT-1998; Homo sapiens. 12-OCT-1999; 21-AUG-2000 20-APR-2000. antagonist. Behan DP, AAY90679; AAY90679

Non-endogenous constitutively activated human G protein-coupled receptors, useful for identifying agonists for use as pharmaceutical agents.

N-PSDB; AAA30759.

Example 1; Page 308-309; 341pp; English.

The invention relates to constitutively active, non-endogenous versions of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-AAY90677 and AAY90683-Y90687), and to DNA encoding them (AAA30709-A30743 and AAA30775-A30779). The mutant proteins of the invention contain a mutation in a portion of the protein comprising intracellular loop 3 (ICS) and transmembrane domain 6 (TM6). A non-endogenous mainto acid, X, is substituted for an endogenous residue in IC3 at a position 16 amino acid N-terminal of an endogenous proline in TM6 to form a sequence X-AAA15-Pro. The endogenous amino acid is selected from Lys, His, Arg or Ala, and is preferably Lys. When the endogenous residue at this position is Lys, this residue is replaced by His, Arg or preferably Ala. The 15

amino acid stretch between the substituted amino acid and the Pro may be endogenous, non-endogenous, or a mixture of endogenous and non-endogenous residues. The constitutively active GPCRs are useful for identifying antagonists, agonists and partial agonists for use as pharmaceutical agents. The mutant proteins are also useful in research settings for elucidating the roles of the receptors in normal and diseased conditions. Antagonists for a particular GPCR are useful for treating diseases and disorders associated with that receptor. Because the novel mutant GPCRs are constitutively active, they can be used directly for screening of compounds without the need for endogenous ligands. The present sequence represents a human wild-type GPCR referred to in an exemplification of the invention 8\$6666666666668

Sequence 300 AA;

240 61 LKAVEALASGAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRP 120 61 LKAVEALASGAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRP 120 CYSWGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAWDPASAG 180 CYSWGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAWDPASAG 180 PARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGGALLTLLLCVGPY 240 NASNVASFLYPNLGGSWRKLGLITGAWSVVLNPLVTGYLGRGPGLKTVCAARTQGGKSQK 300 9 9 1 MDLPPQLSFGLYVAAPALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCSDLLLTVSLP 181 PARFSLSLLLFFLPLATTAFCYVGCLRALARSGLTHRRKLRAAWVAGGALLTLLLCVGPY MDLPPQLSFGLYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCSDLLLTVSLP Gaps ö Length 300; 0; Indels 100.0%; Score 1584; DB 3; 100.0%; Pred. No. 1.6e-149; ive 0; Mismatches 0; Query Match Best Local Similarity 100. Matches 300; Conservative 181 241 121 121 δ 셤 ઠે 셤 à g ઠે 요 ઠે

ABG31106 standard; protein; 300 AA ABG31106; ABG31106
XX
AC ABG3
XX
AC ABG3
XX
DT 21-0
XX
KW Huma
XW Huma
XW G Pr
XW G Pr
XW G Pr
XX
XX
YO D 25-J
XX
XX
PP 25-J
XX
XX
PP 18-C
PP XX
PP 18-C
PP 18-C
PP XX
PP 18-C
PP 18-RESULT

241 NASNVASFLYPNIGGSWRKLGLITGAWSVVLNPLVTGYLGRGPGLKTVCAARTQGGKSQK 300

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(first entry) 21-OCT-2002 Human G protein-coupled receptor GPR40.

Human; GPR40; G protein-coupled; receptor; type 2 diabetes; obesity; antidiabetic; neuroprotective; anorectic; cerobroprotective; Gq; G protein; reporter gene; glucose intolerance; insulin intolerance; neurodegenerative disease; Alzheimer's disease; stroke

Homo sapiens.

WO200257783-A2

25-JUL-2002.

18-DEC-2001; 2001WO-US048985

22-DEC-2000; 2000GB-00031527

(GLAX) GLAXO GROUP LTD. (SMIK) SMITHKLINE BEECHAM PLC.

Tadayyon M; Sauls HR, Muir AI, Ignar DM, Andrews JL, Briscoe CP,

WPI; 2002-599726/64. N-PSDB; ABK90236.

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The invention relates to screening a test compound to determine whether the compound is a GPR40 receptor (G protein-coupled receptor) ligand comprises detecteding whether the test compound competitively inhibits the binding of a fatty acid GPR40 ligand to a GPR40 receptor. Also included are (1) a method of screening a compound for GPR40 antagonist activity, comparising: (a) measuring any detectable signal produced by a reporter gene (comprising: (a) measuring any detectable signal produced by a reporter gene (comprising in the presence of both test compound and agonist; or (c) detecting whether the compound decreases glucose-stimulated insulin release from mammalian parcreatic beta cells in the presence of a GPR40 agonist; comparison of the GPR40 agonist; (2) a method of screening a compound for GPR40 agonist; (2) a method of screening a compound for GPR40 agonist activity, which comprises: (a) detecting any compound for GPR40 agonist activity, which comprises: (a) detecting any compound for GPR40 agonist activity, which comprises: (a) detecting any compound for GPR40 agonist compounds for treating disorders e.g. type 2 diabetes, obesity, glucose-stimulated insulin release from mammalian character, obesity, glucose or insulin intolerance, neurodegenerative compuence compounds for treating disorders e.g. type 2 diabetes, obesity, glucose or insulin intolerance, neurodegenerative compounds compounds for treating disorders e.g. type 2 represents human GPR40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 LKAVEALASGAMPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFFPLGYQAFRRP 120
Identifying GPR40 receptor ligand for treating disorders e.g. obesity, comprises detecting whether the test compound competitively inhibits the binding of a fatty acid GPR40 ligand to a GPR40 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MDLPPQLSFGLYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCSDLLLTVSLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 1584; DB 5; Length 300; 100.0%; Pred. No. 1.6e-149; Ive 0; Mismatches 0; Indels 0.
                                                                                                          Disclosure; Page 48-49; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 300; Conservative
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G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; protein-coupled receptor modulator; antibody; immune-related disease; growth-related disease; cell regeneration-related disease; ADS; cancer; immunological-related cell proliferative disease; autoimmune disease; Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy; esteoporosis; cardiomyopathy; inflammation; crohn; disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; 240 181 PARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGGALLTLLLCVGPY 240 NASNVASFLYPNLGGSWRKLGLITGAWSVVLNPLVTGYLGRGPGLKTVCAARTQGGKSQK 300 PARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGGALLTLLLCVGPY Human G protein-coupled receptor GPR40 protein SEQ ID NO:475. A ABP81994 standard; protein; 300 (first entry) 04-MAR-2003 181 ABP81994; 241 241 RESULT 3 ABP81994 셤 ð 셤 ò

121 CYSWGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAWDPASAG 180

셤

mental retardation, epilepsy, asthma; tuberculosis, obesity, nausea; hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma; (LIFE-) LIFESPAN BIOSCIENCES INC. 19-DEC-2001; 2001WO-US050107 19-DEC-2000; 2000US-0257144P Roush CL, WPI; 2003-046718/04. N-PSDB; ABZ42843. WO200261087-A2 Homo sapiens. 08-AUG-2002 Burmer GC, ulcer.

New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or autoimmune diseases.

Disclosure; Fig 1; 523pp; English.

The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino caids. Also described: (1) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polyapptide in a sample; and (2) an isolated antibody having high specificity and high affinity or andidate particular GPCR. (I) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibody against a particular GPCR, and in the production of specific antibody against a particular GPCR, and in the production of specific antibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for captening immune-related diseases, e.g. AlDS, Alabaimer's disease, call reaging immune-related disease, e.g. AlDS, Alabaimer's disease, atherosclerosis, bacterial, fungal, protozoan or viral infections, atherosclerosis, bacterial, fungal, protozoan or viral infections, osteoporosis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, varial infections and acute disease, parkinson's disease, multiple sclerosis, pain, psoriasis, canxety, depression, schizophrenia, dementia, memory consession, phypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or sepilepsy, asthma, tuberculosis, obesity, nausea, hypertension, hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or used in immunoassays and immunodiagnosis. ABZ42253 to ABZ42869 encode GPCR proteins given in ABPB1675 to ABBP2018, which are used in the present invention

Sequence 300 AA;

LKAVEALASGAWPLPASLCPVFAVAHFPPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRP 120 61 LKAVEALASGAMPLPASLCPVFAVAHFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRP 120 CYSWGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAWDPASAG 180 CYSWGVCAAIWALVLCHIGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAWDPASAG 180 9 1 MDLPPQLSFGLYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCSDLLLTVSLP Gaps ; 0 100.0%; Score 1584; DB 6; Length 300; 100.0%; Pred. No. 1.6e-149; ive 0, Mismatches 0; Indels 0 Matches 300; Conservative Local Similarity 61 121 Query Match Š 윱 8 셤 ò 요 181 PARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGGALLTLLLCVGPY 240

δ

300 241 NASNVASFLYPNLGGSWRKLGLITGAMSVVLNPLVTGYLGRGPGLKTVCAARTQGGKSQK 300 241 NASNVASFLYPNLGGSWRKLGLITGAWSVVLNPLVTGYLGRGPGLKTVCAARTQGGKSQK ò

RESULT 4 ADB61404

ADB61404 standard; protein; 300 AA

ADB61404;

04-DEC-2003 (first entry)

Human GPR40 protein.

fatty acid; eicosanoid-binding G-protein coupled receptor; GFR40; antidiabetic; anabolic; neuroprotective; nephrotropic; ophthalmological; antialipaemic; dermatological; antiarteriosclerotic; antiarthritic; osteopathic; thrombolytic; noctropic; anorectic; hypotenalve; cytostatic; diabetes; ketosis; acidosis; diabetic neuropathy; diabetic nephropathy; bone diabetic retinopathy; hyporlipaemia; skin disease; arthritis; bone disease; arteriosclerosis; thrombosis; hyportension; indigestion; memory loss; obesity; hypoglycaemia; edema; insulin resistance; insulin allergy; fat metabolism disorder; cancer; human.

Homo sapiens.

WO2003068959-A1.

21-AUG-2003.

13-FEB-2003; 2003WO-JP001483.

14-FEB-2002; 2002JP-00037131. 12-JUL-2002; 2002JP-00204163. 12-NOV-2002; 2002JP-00328696.

22-JAN-2003; 2003JP-00014032 (TAKE) TAKEDA CHEM IND LTD Ito Y, Kobayashi M, Tanaka H, Okubo S; Kawamata Y, Ogi K, Harada M, Fukusumi S; Новоуа М, Kizawa H, ŝ Pujii R, Hinuma

WPI; 2003-671661/63. N-PSDB; ADB61403. Fatty acid and elcosanoid-binding G-protein coupled receptor protein GPR40 for control of pancreatic function and treatment of diabetes.

Claim 34; Page 235-236; 257pp; Japanese.

The invention relates to a novel screening method comprising a fatty acid and eicosanoid-binding G-protein coupled receptor protein, GPR40, originating in mouse. Tat, crab-eating workey and hamster (sequences fully defined in the specification), equivalent proteins of similar activity, and peptides containing partial sequences of the GPR40 protein. The novel fatty acid and GPR40 protein and thehr compositions have the following activities: antidiabetic, anabolic, neuroprotective, nephrotropic, ophthalmological, antilipaemic, dermatological, antiarterioscherotic, antiarthritic, osteopathic, thrombolyric, noctropic, anorectic, hypotensive, and cytostatic. The novel fatty acid and eicosanoid-binding G-protein coupled receptor protein, GPR40, and diagnosis of diabetes, ketosis, acidosis, diabetic neuropathy, diabetic retinopathy, diabetic retinopathy, diabetic retinopathy, diabetic retinopathy, diabetic retinopathy, hyporlipaemia, skin diseases, arthritis, bone diseases, arteriosclerosis, thrombosis, hypertension, indigestion, memory loss, obesity, hypoglycaemia, edema, insulin cresistance, insulin allergy, fat metabolism disorders and cancer. This sequence represents a human GPR40 protein of the invention.

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Homo sapiens
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                                                                                                                                                                                                                                                                 The invention relates to a method for treating a non-endogenous, constitutively active version of an endogenous human G protein-coupled receptor (GPCR) that has a transmembrane-6 (TM6) region and an intracellular-3 (TG3) region, by substituting a specific amino acid in the TM6 region with a different amino acid, and testing for constitutive activity. The method is useful for creating a constitutively active
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                                                                                                                            CYSWGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAWDPASAG
                                                                                                                                                                        CYSWGVCAAIWALVLCHIGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAWDPASAG
                                                                                MDLPPQLSFGLYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCSDLLLTVSLP
                                                                                                              LKAVEALASGAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRP
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                   100.0%; Score 1584; DB 7; Length 300; 100.0%; Pred. No. 1.6e-149; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                         Human G protein-coupled receptor (GPCR) polypeptide #36,
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98US-0090783P.
98US-0095677P.
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                                            Matches 300; Conservative
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N-PSDB; ADC22768.
                                Local Similarity
Sequence 300 AA
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26-JUN-1998;
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version of an endogenous human GPCR that comprises a transmembrane 6 region and an intracellular loop 3 region. The altered human GPCR polypeptides are useful for screening test compounds for identification of inverse agonists or partial agonists of GPCR polypeptides, which may have therapeutic uses. The altered GPCRs may also be used in vivo or in vitro in biological research. A nucleic acid encoding the altered GPCR may be used to create a transgenic animal expressing the altered GPCR. The method allows screening for compounds that modulate the activity of a human G protein-coupled receptor without the need for provision of a ligand for the receptor. This is particularly useful in allowing screening of compounds against orphan receptors for which no ligand is currently known. This sequence represents a human GPCR polypeptide of the
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intracellular loop 3; transmembrane domain 6; drug screening; agonist;
antagonist; mutant; mutein.
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N-PSDB; AAA30776.
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29-APR-2003

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The invention branch to constitutively active, non-endogenous versions of endogenous human orphan G protein-coupled receptors (GCRS, AAY90643-AAY90677 and AAY90683-Y90687), and to DNA encoding them (AAA30709-A30743) and AAA30775-A30779). The mutant proteins of the invention contain a mutation in a portion of the proteins of the invention contain a mutation in a portion of the proteins of the invention contain a mutation in a portion of the proteins of the invention contain a contain a mutation in a portion of the invention of the invention of amino acid stretched for an endogenous residue in TM6 to form a sequence X-CC (AA)15-Pro. The endogenous amino acid is preferably Lys. When the endogenous residue at this position is Lys, this residue is replaced by His, Arg or preferably Ala. The 15 amino acid stretch between the substituted amino acid and the Pro may be endogenous, non-endogenous, or a mixture of endogenous and non-endogenous cresidues. The one-integration of partial agonists for use as pharmaceutical conditions. The mutant proteins are also useful for treating for a elucidating the roles of the receptors in normal and diseased conditions. Antagonists for a particular GPCR are useful for treating diseases and disorders associated with that receptor. Because the novel mutant GPCRs are constitutively active, they can be used directly for screening of compounds without the need for endogenous ligands. Sequences AAY90643-CC AAY90677 and AAY90663-Y90687 the mutant human GPCRs of the invention
                                                                                                                                                                                    The invention relates to constitutively active, non-endogenous versions
Non-endogenous constitutively activated human G protein-coupled receptors, useful for identifying agonists for use as pharmaceutical
                                                                                                                           Example 2; Page 325-326; 341pp; English.
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Sequence 300 AA;

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61 LKAVEALASGAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRP 120
                                                                                                                                                                   CYSWGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAWDPASAG 180
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Length 300;
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99.7%; Score 1579; DB 3; 99.7%; Pred. No. 5.1e-149; iive 0; Mismatches 1;
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Human G protein-coupled receptor (GPCR) polypeptide #76.
            ADC22791 standard; protein; 300 AA
                                       18-DEC-2003 (first entry)
                          ADC22791;
     RESULT 7
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241 ADB61416 ID ADB6 RESULT Human, G protein-coupled receptor; GPCR; transmembrane-6 region; TM6; intracellular-3 region; IC3; receptor.

Homo sapiens US6555339-B1

ADB61416 standard; protein; 300 AA

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The invention relates to a method for treating a non-endogenous, constitutively active version of an endogenous human G protein-coupled receptor (GPCR) that has a transmembrane-6 (TMG) region and an intracellular-3 (IC3) region, by substituting a specific amino acid in intracellular-3 (IC3) region, by substituting a specific amino acid in the TMG region with a different amino acid, and testing for constitutive activity. The method is useful for creating a constitutively active version of an endogenous human GPCR that comprises a transmembrane 6 region and an intracellular loop 3 region. The altered human GPCR colypeptides are useful for screening test compounds for identification of inverse agonists or partial agonists of GPCR polypeptides, which may have therapeutic uses. The altered GPCRs may also be used in vivo or in viro in biological research. A nucleic acid encoding the altered GPCR may be used to create a transgenic animal expressing the altered GPCR conversed and allows screening for compounds that modulate the activity of a ligand for the receptor. This is particularly useful in allowing corrections of a correction of a ligand for compounds against orphan receptors for which no ligand is currently known. This sequence represents a human GPCR polypeptide of the
                                                                                                                                                                                                                                                                                                                          Creating a constitutively active version of an endogenous human G protein coupled receptor (GPCR) comprises substituting a specific amino acid in the transmembrane-6 region with a different amino acid, and testing for
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98US-00060188.
98US-0090783P.
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Best Local Similarity 99.7
Matches 299; Conservative
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                                        13-OCT-1998;
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26-JUN-1998;
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(first entry)

protein.

Monkey GPR40 04-DEC-2003 Hinuma S, Primates. Fujii R, ADB61416;

fatty acid; eicosanoid-binding G-protein coupled receptor; GPR40; antidiabetic; anabolic; neuroprotective; nephrotropic; opthalmological; antilipaemic; dermatological; antiarteriosclerotic; antiarthritic; osteopathic; thrombolytic; noortopic; anorectic; hypotensive; cytostatic; diabetic retinopathy; diabetic neuropathy; diabetic nephropathy; diabetic nephropathy; byperlipaemia; skin disease; arthritis; bone disease; arteriosclerosis; thrombosis; hyportrension; indigestion; memory loss; obesity; hypoglycemia; edema; insulin resistance; insulin allergy; fat metabolism disorder; cancer; monkey. Ito Y, Kobayashi M, Tanaka H, Okubo S Kawamata Y, Ogi K, Harada M, Fukusumi 14-FEB-2002; 2002JP-00037131. 12-JUL-2002; 2002JP-00204163. 12-NOV-2002; 2002JP-0032B696. 22-JAN-2003; 2003JP-00014032. 13-FEB-2003; 2003WO-JP001483 (TAKE) TAKEDA CHEM IND LTD Новоуа М, Kizawa H, WPI; 2003-671661/63 N-PSDB; ADB61417. WO2003068959-A1. 21-AUG-2003.

Fatty acid and eicosanoid-binding G-protein coupled receptor protein GPR40 for control of pancreatic function and treatment of diabetes.

Claim 1; Page 240-241; 257pp; Japanese.

The invention relates to a novel screening method comprising a fatty acid and elcosanoid-binding G-protein coupled receptor protein, GPR40, originating in mouse, rat, crab-eating monkey and hamster (sequences fully defined in the specification), equivalent proteins of similar activity, and peptides containing partial sequences of the GPR40 protein. The novel farty acid and GPR40 protein and their compositions have the collowing activities: antidiabetic, anabolic, neuroprotective, ephrotropic, ophthalmological, antilipaemic, dermatological, nethrotropic, antiatrhitic, osteopathic, thrombolytic, notropic, antiatrhitic, osteopathic, thrombolytic, notropic, ancestic, hypotensive, and cytostatic. The novel fatty acid and elcosanoid-binding G-protein coupled receptor protein, GPR40, and further compositions can be used in the treatment, prevention and funganosis of diabetics retinopathy, hyperlipaemia, skin diseases, arthritis, bone diseases, arteriosclerosis, thrombosis, hypertension, arthritis, bone diseases, arteriosclerosis, thrombosis, hypertension, resistance, insulin allergy, fat metabolism disorders and cancer. This sequence represents a monkey GFR40 protein of the invention.

Sequence 300 AA;

ö Gaps ő Length 300; 10; Indels Score 1519; DB 7; Pred. No. 4.9e-143; 0; Mismatches 10; 95.98; Query Match
Best Local Similarity 96.7
Matches 290; Conservative

61 LKAVEALASGAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRP 120

9 1 MDLPPQLSFALYVAAFALGFPLNVLAIRGARAHARRRITPSLVYALNLGCSDLLLTVSLP

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MDLPPQLSFGLYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCSDLLLTVSLP

180 240 300 240 241 NASNVASFLNPNIGGSWRKZGLITGAWSVVLNPLVTGYLGRGPGLKTVCAARTQGSTSQK 300 241 NASNVASFLYPNLGGSWRKLGLITGAWSVVLNPLVTGYLGRGPGLKTVCAARTQGGKSQK CYSWGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAWDPASAG PARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGGALLTLLLCVGPY 181 61 121 ò 요 ò 셤 ò 셤

ABG31107 standard; protein; 300 AA. RESULT 9 ABG31107

ABG31107;

(first entry) 21-OCT-2002 Mouse G protein-coupled receptor GPR40.

Mouse; GPR40; G protein-coupled; receptor; type 2 diabetes; obesity; antidiabetic; neuroprotective, annectic; cerobroprotective; Gq; G protein; reporter gene; glucose intolerance; insulin intolerance; neurodegenerative disease; Alzheimer's disease; stroke.

Mus sp.

WO200257783-A2

25-JUL-2002.

18-DEC-2001; 2001WO-US048985.

22-DEC-2000; 2000GB-00031527.

GLAX) GLAXO GROUP LTD.

SMIK) SMITHKLINE BEECHAM PLC.

Ignar DM, Muir AI, Sauls HR, Tadayyon M;

WPI; 2002-599726/64. N-PSDB; ABK90237.

Andrews JL, Briscoe CP,

Identifying GPR40 receptor ligand for treating disorders e.g. obesity, comprises detecting whether the test compound competitively inhibits the binding of a fatty acid GPR40 ligand to a GPR40 receptor.

Disclosure; Page 51; 53pp; English.

The invention relates to screening a test compound to determine whether the compound is a GPR40 receptor (G protein-coupled receptor) ligand computies detecting whether the test compound competitively inhibits the binding of a fatty acid GPR40 ligand to a GPR40 receptor. Also included are (1) a method of screening a compound for GPR40 antagonist activity, comprishing; (a) measuring any detectable signal produced by a reporter gene (comprishing a reporter gene under the control of G protein GG responsive transcriptional element); (b) detecting a decrease in reporter gene expression in the presence of both test compound and agonist; or (c) detecting whether the compound decreases glucose-stimulated insulin clease from mammalian pancreatic beta cells in the presence of a GPR40 agonist, compared to glucose-stimulated insulin release that would occur agonist, compared to glucose-stimulated insulin release that would occur agonist, compared to glucose-stimulated insulin release that would occur compound for GPR40 agonist activity, which comprises: (a) detecting any reporter gene expression; or (b) detecting whether the compound binds to GPR40 and increases glucose-stimulated insulin release from mammalian pancreatic beta cells. The method is useful for identifying GPR40 antagonist or agonist compounds for treating disorders e.g. type 2

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                                                                                                                                      Gaps
diabetes, obesity, glucose or insulin intolerance, neurodegenerative disease (e.g. Alzheimer's disease) or stroke. The present sequence represents mouse GPR40
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                                                                                                     Length 300,
                                                                                                                                      34; Indels
                                                                                                     84.2%; Score 1333; DB 5;
83.0%; Pred. No. 1.8e-124;
                                                                                                                                    Matches 249; Conservative 17; Mismatches
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fatty acid; eicosanoid-binding G-protein coupled receptor; GPR40; antidiabetic; anabolic; neuroprotective; nephrotropic; ophthalmological; antilipaemic; dermatological, antiartericic; antiarthritic; osteopathic; thrombolytic; nootropic; anorectic; hypotensive; cytostatic; diabetic; thrombolytic; nootropic; anorectic; hypotensive; cytostatic; diabetic retinopathy; diabetic nephropathy; byperlipaemia; skin disease; arthritis; bone disease; arteriosclerosis; thrombosis; hypotension; indigestion; memory loss; obesity; hypoglycaemia; edema; insulin resistance; insulin allergy; fat metabolism disorder; cancer; mouse; murine.
ADB61400
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14-FEB-2002; 2002JP-00037131. 12-JU-2002; 2002JP-00204163. 12-NOV-2002; 2002JP-00328696. 22-JAN-2003; 2003JP-00014032. 13-FEB-2003; 2003WO-JP001483 WO2003068959-A1 21-AUG-2003

(TAKE) TAKEDA CHEM IND LTD

, Okubo S; Fukusumi S , Tanaka H, Harada M, F Ito Y, Kobayashi M, Kawamata Y, Ogi K, H Hosoya M, Kizawa H, Hinuma S, Pujii R,

WPI; 2003-671661/63. N-PSDB; ADB61401.

Fatty acid and eicosanoid-binding G-protein coupled receptor protein

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The invention relates to a novel screening method comprising a fatty acid and elcosanoid-binding G-protein coupled receptor protein, GPR40, originating in mouse, rat, crab-eating monkey and hamster (sequences think) defined in the specification), equivalent proteins of similar activity, and peptides containing partial sequences of the GPR40 protein. The novel fatty acid and GPR40 protein and their compositions have the following activities: antidiabetic, anabolic, neuroprotective, nephrotropic, ophthalmological, antilipaemic, dermatological, antiarthritic, osteopathic, thrombolytic, nootropic, anorectic, hypotensive, and cytostatic. The movel fatty acid and eicosanoid-binding G-protein coupled receptor protein, GPR40, and diagnosis of diabetes, ketosis, acidosis, diabetic neuropathy, diabetic nephropathy, diabetic retinopathy, hyperlipaemia, skin diseases, compositions can be used in the treatment, prevention and diagnosis of diabetes retinopathy, hyperlipaemia, skin diseases, arthritis, bone diseases, arteriosclerosis, thrombosis, hypertension, indigestion, memory loss, obesity, hypoglycaemia, edema, insulin allergy, fat metabolism disorders and cancer. This sequence represents a mouse GPR40 protein of the invention.
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GPR40 for control of pancreatic function and treatment of diabetes
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                                          Claim 1; Page 230-231; 257pp; Japanese.
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ADB61402 standard; protein; 300 AA (first entry) 04-DEC-2003 ADB61402;

RESULT 11 ADB61402 Rat GPR40 protein.

antidiabetic; anabolic; neuroprotective; nephrotropic; ophthalmological; antilipaemic; dermatological; antiarteriosclerotic; antiarthitic; osteopathic; thrombolytic; nootropic; anorectic; hypotensive; cytostatic; diabetis; ketosis; acidosis; diabetic neuropathy; diabetic nephropathy; diabetic retinopathy; hyperlipaemia; skin disease; arthritis; mone disease; arthritis; memory loss; obesity; hypoglycaemia; edema; insulin resistance; insulin allergy; fat metabolism disorder; cancer; rat. fatty acid; eicosanoid-binding G-protein coupled receptor; GPR40;

Rattus

WO2003068959-A1

(first entry)

04-DEC-2003

ADB61428;

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The invention relates to a novel screening method comprising a fatty acid and elcosanoid-binding G-protein coupled receptor protein, GPR40, originating in mouse, rat, crab-eating monkey and hamater (sequences cully defined in the specification), equivalent proteins of similar activity, and peptides containing partial sequences of the GPR40 protein. The novel fatty acid and GPR40 protein and their compositions have the collowing activities: antidiabetic, anabolic, neuroprotective, nephrotropic, ophthalmological, antidiabetic, anabolic, dermatological, antiatrerioeclerotic, antiatrhitic, osteopathic, thrombolytic, notropic, anorectic, hypotensive, and cytostatic. The novel fatty acid and elcosanoid-binding G-protein coupled receptor protein, GPR40, and functions can be used in the treatment, prevention and funganosis of diabeters, ketosis, acidosis, diabetic neuropathy, diabetic retinopathy, hyperlipaemia, skin diseases, arthitis, bone diseases, arteriosclerosis, thrombosis, hypertension, arthitis, bone diseases, arteriosclerosis, thrombosis, hypertension, resistance, insulin allergy, fat metabolism disorders and cancer. This sequence represents a rat GPR40 protein of the invention.
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Fukusumi S;
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81.7%; Pred. No. 3.6e-123;
ive 19; Mismatches 36; Indels
                                                                                                                                                                                                                                      , Tanaka H,
Harada M, 1
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Kawamata Y, Ogi K, F
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                                                                                                14-FEB-2002; 2002JP-00037131.
12-JU-2002; 2002JP-00204163.
12-NOV-2002; 2002JP-00328696.
22-JAN-2003; 2003JP-00014032.
                                                         13-FEB-2003; 2003WO-JP001483
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Kizawa H, }
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                    21-AUG-2003
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61 LKAVEALASGAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRP 120
                                                                                                   61 LKAVEALASGVWPLPLPFCPVFALAHFAPLYAGGGFLAALSAGRYLGAAFPFGYQAIRRP 120
                                                                                                                                                         121 CYSWGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAWDPASAG 180
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                    1 MDLPPQLSFALYVSAFALGFPLNLLAIRGAVSHAKLRLTPSLVYTLHLACSDLLLAITLP
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ADB61428 standard; protein; 300 AA

RESULT 12 ADB61428

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The invention relates to a novel screening method comprising a fatty acid and elcosanoid-binding G-protein coupled receptor protein, GPR40, coriginating in mouse, rat, crab-eating monkey and hamster (sequences tully defined in the specification), equivalent proteins of similar activity, and peptides containing partial sequences of the GPR40 protein. The novel fatty acid and GPR40 protein and thehri compositions have the following activities: antidiabetic, anabolic, neuroprotective, compuroropic, ophthalmological, antilipaemic, dermatological, antiarterisoclerotic, antiarthritic, osteopathic, thrombolytic, noctropic, anorectic, hypotensive, and cytostatic. The novel fatty acid and elcosanoid-binding G-protein coupled receptor protein, GPR40, and citater compositions can be used in the treatment, prevention and diagnosis of diabetic retinopathy, hyperlipaemia, skin diseases, compuropathy, diabetic retinopathy, hyperlipaemia, skin diseases, continitis, bone diseases, arteriosclerosis, thrombools, hypertension, indigestion, memory loss, obesity, hyposlycaemia, edema, insulin allersy, fat metabolism disorders and cancer. This creatstance, insulin allersy, fat metabolism disorders and cancer. This
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                                                                                                                                      antidiabetic; anabolic; neuroprotective; nephrotropic; ophthalmological; antilipaemic; dermacological; antiarteriosclerotic; antiarthritic; osteopathic; thrombolytic; nootropic; anorectic; hypotensive; cytostatic; diabetes; ketosis; acidosis; diabetic neuropathy; diabetic nephropathy; diabetic nephropathy; diabetic retinopathy; hyperlipaemia; skin disease; arthritis; memory loss; obesity; hypoglycaemia; edema; insulin resistance; insulin allergy; fat metabolism disorder; cancer; hamster.
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Fukusumi S;
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                                                                                                                     fatty acid; eicosanoid-binding G-protein coupled receptor;
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81.8%; Score 1295; DB 7; Length 3:
Best Local Similarity 80.7%; Pred. No. 1.1e-120;
Matches 242; Conservative 21; Mismatches 37; Indels
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Kawamata Y, Ogi K, Harada M, F
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12-NOV-2002; 2002JP-00328696.
22-JAN-2003; 2003JP-00014032.
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                                                                                 Hamster GPR40 protein
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N-PSDB; ADB61429.
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                                                                                                                                                                                                                                                                                                                                                                       WO2003068959-A1.
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                           NASNVASFLYPNIGGSWRKLGLITGAWSVVLNPLVTGYLGRGPGLKTVCAARTQGGKSQK 300
                                                                                                   VKAVEALASGAWPLPLPLCPVFVLVHFAPLYAGGGFLAALSAGRYLGAAFPFGYQAVRRP 120
                                                                                                                                                                                                                                GPR 42; G-protein coupled receptor 42; human; drug screening; dyslipidaemia; coronary heart disease; atherosclerosis; thrombosis; obesity; angina; kidney failure; peripheral vascular disease; stroke; diabetes; metabolic syndrome; syndrome x; antilipaemic; cardiant; antiatherosclerotic; thrombolytic; anorectic; antianginal; nephrotropic; vasotropic; cerebroprotective; antidiabetic; therapy.
                                                                CYSWGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAWDPASAG
                                                       PARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGGALLTLLLCVGPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                an agent for the modulation of G-protein coupled or the treatment of disease i.e. dyslipidemia or t
                                                                                                                                                                                                              Human G-protein coupled receptor GPR 42.
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/label= Transmembrane
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/label= Transmembrane
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/label= Transmembrane
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                                                                                                                                                                                                                                                                                                                 location/Qualifiers
                                                                                                                                                       AAB82759 standard; protein; 346 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-PEB-2001; 2001WO-GB000684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-FEB-2000; 2000GB-00003900, 22-MAR-2000; 2000GB-00007015.
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/label= Tr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identification of ar
receptor useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brown AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAH26460.
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                                                                                                                                                                                                                                                                                                Homo sapiens
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61
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Domain
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AAB82759
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The present sequence is that of human G-protein coupled receptor 42 (GPR 42). The invention is based on the finding that expression of GPR 42 and

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GPR 41 (see AAB82758) is restricted to adipose tissue. GPR 41 or GPR 42 may therefore be used as a screening target for the identification and development of novel pharmaceutical agents for use in inhibiting 11pplysis. Methods are claimed for identifying agents that modulate GPR 41 or GPR 42 activity, involving: (1) contacting a test agent with GPR 41 or GPR 42 or a variant polypeptide capable of coupling to a G-protein, or GPR 42 or a variant polypeptide capable of coupling to a G-protein, thereby determining whether the test agent modulates activity. Such agents, which may be an activator of GPR 41 or GPR 42, an inhibitor of 1holysis, or a polynucleotide encoding GPR 41, GPR 42 or variant polypeptide, are useful for the treatment of dyslipidaemia, coronary heart disease, attended encoding GPR 41, angina, chronic metabolic syndrome (syndrome X) (all claimed)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 DLLLLLELPRRWVEAANGMHWPLPFILCPLSGFIPFTTIYLTALFLAAVSIERFLSVAHP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112 LGYQAFRRPCYSWGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVC- 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           171 LEAWDP--ASAGPARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGG 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52 DLLLTVSLPLKAVEALASGAWPLPASLCPVPAVAHFFPLYAGGGFLAALSAGRYLGAAFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 protein-coupled receptor; GPCR; constitutively active;
intracellular loop 3; transmembrane domain 6; drug screening; agonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MDLPPQLS------FGLYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MDTGPDQSYPSGNHWFVFSVYLLTPLVGLPLNLLALVVFVGKLRCRPVAVDVLLLNLTAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         230 TLINFLVCFGPYNVSHVVGYI---CGESPVWRIYVTLLSTLNSCVDPFVYYFSSSG 282
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                28;
                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 34.1%; Pred. No. 6.8e-28;
Matches 101; Conservative 38; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                                                                                                                  23.1%; Score 366; DB 4; 34.1%; Pred. No. 6.8e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human G protein-coupled receptor GPR41.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US023938
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chalmers DT,
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N-PSDB; AAA30762.
                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                        Sequence 346 AA;
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18. .41
/label= Transmembrane

Location/Qualifiers

Homo sapiens.

Domain Domain Domain Domain Domain Domain Domain

52. .73 /label= Transmembrane

Transmembrane Transmembrane Transmembrane

88. .111 /label= T

.153

229. .250 /label= Transmembrane

188. .21; /label= ? label=

/label= Transmembrane

WO200161359-A2

23-AUG-2001

19-FEB-2001; 2001WO-GB000684. 18-FEB-2000; 2000GB-00003900. 22-MAR-2000; 2000GB-00007015.

(GLAX) GLAXO GROUP LTD.

WPI; 2001-536581/59. Wise A, Brown AJ;

N-PSDB; AAH26459

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The invention relates to constitutively active, non-endogenous versions of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-AAY90677 and AAY906677 and AAY90677). The mutant proteins of the invention contain a mutation in a portion of the protein comprising intracellular loop 3 (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X, is substituted for an endogenous residue in IC3 at a position 16 amino acids N-terminal of an endogenous residue in IC3 at a position 16 amino acids N-terminal of an endogenous proline in TM6 to form a sequence X-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg or Ala, and is preferably Lys. When the endogenous residue at this position is Lys, this residue is replaced by His, Arg or preferably Ala. The 15 amino acid stretch between the substituted amino acid and the Pro may be endogenous, non-endogenous, or a mixture of endogenous and non-endogenous cresidues. The constitutively actival agonists for use as pharmaceutical agenists, agonists and partial agonists for use as pharmaceutical agents. The mutant proteins are also useful in research settings for clucidating the roles of the receptors in normal and diseased conditions. Antagonists for a particular GPCRs are useful for treating diseases and diseases and diseases associated with that receptors. Because the novel mutant GPCRs are constitutively active, they can be used directly for screening of compounds without the need for endogenous ligands. The present sequence represents a human wild-type GPCR referred to in an exemplification of
Non-endogenous constitutively activated human G protein-coupled receptors, useful for identifying agonists for use as pharmaceutical
                                                                                                                             Example 1; Page 310-311; 341pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the invention
                                                                      agents.
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Sequence 346 AA;

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52 DLLLTVSLPLKAVEALASGAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFP 111
                                                                                                                                                                                                             61 DLLLLLELPFRAVEAANGMHWPLPFILCPLSGFIFFTTIYLTALFLAAVSIERFLSVAHP 120
                                                                                                                                                                                                                                                                          112 LGYQAFRRPCYSWGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCL 171
                                                                                                                                                                                                                                                                                                   172 EAW---DPASAGPARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGG 228
                                                                                                                                                                                                                                                                                                                                                                                          21
                                                                                                                                     1 MDTGPDQSYFSGNHWFVFSVYLLTFLVGLPLNLLALVVFVGKLQRRPVAVDVLLLANLTAS 60
                                                                                           1 MDLPPQLS------FGLYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCS
                                                24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  230 TLLNFLVCFGPYNVSHVVGYICGE-SPAMRIYVTLLSTLNSCVDPFVYYPSSG 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                        229 ALLILLCVGPYNASNVASFLYPNLGGSWRKLGLITGAWSVVLNPLVTGYLGRG 282
21.9%; Score 347; DB 3; Length 346; 32.3%; Pred. No. 5.4e-26; ive 41; Mismatches 134; Indels ;
  Query Match
Best Local Similarity 32.3
Matches 95; Conservative
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Identification of an agent for the modulation of G-protein coupled receptor useful for the treatment of disease i.e. dyslipidemia or stoke.

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The present sequence is that of human G-protein coupled receptor 41 (GPR 41). The invention is based on the finding that expression of GPR 41 and GPR 42 (see AAB82759) is restricted to adipose tissue. GPR 41 or GPR 42 may therefore be used as a screening target for the identification and development of novel pharmaceutical agents for use in inhibiting closed are claimed for identifying agents that modulate GPR 11polysis. Methods are claimed for identifying agents that modulate GPR 41 or GPR 42 or a variant polypeptide capable of coupling to a G-protein; or GPR 42 or a variant polypeptide capable of coupling to a G-protein; and (2) monitoring for GPR 41 or GPR 42 activity in the presence of a G-protein, thereby determining whether the test agent modulates activity. Such agents, which may be an activator of GPR 41, GPR 42, an inhibitor of lipolysis, or a polynucleotide encoding GPR 41, GPR 42 or variant polypeptide, are useful for the treatment of dysliphdaemar, coronary heart disease, atheroselerosis, thrombosis or obesity, angina, chronic renal failure, peripheral vascular disease, stroke, type II diabetes or metabolic syndrome (syndrome X) (all claimed)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DILLTVSLPLKAVEALASGAMPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFP 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 DILILIEPPFRAVEAANGMHWPLPFILCPISGFIFFTTIYLTALFLAAVSIERFLSVAHP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 7; Page 44-46; 53pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 346 AA;
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GPR 41; G-protein coupled receptor 41; human; drug screening; dyslipidaemia; coronary heart disease; atherosclerosis; thrombosis; obesity; angina; kidney failure; peripheral vascular disease; stroke; diabetes; metabolic syndrome; syndrome x, antilipaemic; cardiant; antiatherosclerotic; thrombolytic; anorectic; antianginal; nephrotropic; vasotropic; cerebroprotective; antidiabetic; therapy.

Human G-protein coupled receptor GPR 41.

(first entry)

29-OCT-2001 AAB82758;

AAB82758 standard; protein; 346 AA

RESULT 15

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121 LWYKTRPRLGQAGLVSVACWLLASAHCSVVYVIEFSGD-ISHSQGTNG------TCY 170
                        172 EAW---DPASAGPARFSLSLLLFPLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGG 228
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Search completed: April 29, 2004, 12:10:03 Job time : 61 secs

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Compugen Ltd.
version 5
GenCore (c) 1993
       Copyright
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OM protein - protein search, using sw model

April 29, 2004, 12:07:54 ; Search time 20 Seconds (without alignments) 1442.873 Million cell updates/sec Run on:

US-10-202-687-2 1584 Title: Perfect score:

1 MDLPPQLSFGLYVAAFALGF.....RGPGLKTVCAARTQGGKSQK 300 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 78:*
1: Dir1:*
2:. pir2:*
3: pir3:*
1: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	G protein-coupled	G protein-coupled	G protein-coupled	G protein-coupled	thrombin receptor	thrombin receptor	alpha-thrombin rec	somatostatin recep	interleukin-8 rece	thrombin receptor	interleukin-8 rece		G protein-coupled	G protein-coupled	interleukin-8 rece	somatostatin recep	somatostatin recep	G protein-coupled	G protein-coupled	G protein-coupled		G protein-coupled	P-2U nucleotide re	G protein-coupled	macrophage inflamm	interleukin-8 rece	chemokine (C-C) re	ATP receptor P2u -	brain-specific som
SUMMARIES	QI	JC5714	JC5716	JC5715	JC5717	151667	A37912	S17148	157940	JQ1231	A43448	A53752	JC4800	I55450	S68207	A39445	157955	JN0763	153033	A57641	JC5277	S27357	B57641	A54946	868679	149339	A53611	A45177	A47556	A47249
	ОВ	~	~	~	~	~	~	~	7	~	~	~	7	~	~	~	~	~	~	~	~	Н	~	~	~	~	~	~	N	7
	Length	300	346	346	330	420	425	427	363	355	432	358	328	328	362	350	363	364	354	362	359	352	362	375	365	355	360	355	373	384
de	Query	100.0	23.1	21.9	21.0	15.4	14.4	13.4	13.0	12.9	12.9	12.7	12.5	12.5	12.3	12.3	12.2	12.2	12.0	•	•	11.9	11.8	11.7	11.6	11.5	11.5		11.3	11.3
	Score	1584	366	347	332	244	228	213	205.5	204.5	204	201	198.5	197.5	195.5	194.5	194	194	190.5	190.5	189.5	188.5	186.5	186	184	182.5	182.5	180.5	179	179
	Result No.	7	7	m	4	2	9	7	89	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

G protein-coupled	G protein-coupled	somatostatin recep	kappa opioid recep	opioid receptor ho	G protein-coupled	G protein-coupled	G protein-coupled	bradykinin Bl_rece	heptahelical P2Y5-	interleukin-8 rece	delta opioid recep	G protein-coupled	somatostatin recep	G protein-coupled	intron 17 purinerg
B45680	JC5653	JN0605	149022	JC2421	156520	868208	150241	S60024	JC5549	S42096	B48227	S32785	JC4629	G02064	T09508
N	N	~	N	7	~	~	~	~	~	~	~	7	7	~	7
361	361	388	367	367	367	365	308	352	370	356	372	374	384	360	344
11.2	11.2	11.1	11.0	11.0	11.0	10.9	10.9	10.9	10.9	10.8	10.8	10.8	10.8	10.8	10.7
178 11.2				173.5 11.0								171.5 10.8		170.5 10.8	

ALIGNMENTS

RESULT 1

JC5714
G protein-coupled receptor 40 - human
C;Species: Homo sapiens (man)
C;Date: 03-Dec-1997 #sequence revision 23-Jan-1998 #text change 21-Jul-2000
C, Accession: JC5714
R;Sawzdargo, M.; George, S.R.; Nguyen, T.; Xu, S.; Kolakowski Jr., L.F.; O'Dowd, B.F.
Biochem. Biophys. Res. Commun. 239, 543-547, 1997
A; Title: A cluster of four novel human G protein-coupled receptor genes occurring in clos
A; Reference number: JC5714; MUID: 98008875; PMID: 9344866
A;Accession: JC5714
A;Status: nucleic acid sequence not shown
A; Molecule type: mRNA
A;Residues: 1-300 <saw></saw>
A; Cross-references: GB: AF024687; NID: 92612945; PIDN: AAB86710.1; PID: 92612946
C;Superfamily: G protein-coupled receptor 43
C;Keywords: glycoprotein; lipoprotein; thiolester bond
F;13-32/Domain: transmembrane #status predicted <tm1></tm1>

F;43-64/Domain: transmembrane #status predicted <TM2>
F;83-104/Domain: transmembrane #status predicted <TM3>
F;125-144/Domain: transmembrane #status predicted <TM4>
F;184-206/Domain: transmembrane #status predicted <TM4>
F;184-206/Domain: transmembrane #status predicted <TM5>
F;222-243/Domain: transmembrane #status predicted <TM6>
F;252-260/Domain: transmembrane #status predicted <TM6>
F;255-260/Domain: transmembrane #status predicted <TM6>
F;255,165/Binding site: carbohydrate (Asn) (covalent) #status predicted F;289/Binding site: palmitate (Cys) (covalent) #status predicted

Gaps ö Length 300; 0; Indels ; Score 1584; DB 2; ; Pred. No. 2.8e-125; 0; Mismatches 0; 100.0%; Query Match 100. Best Local Similarity 100. Matches 300; Conservative

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9 9 1 MDLPPQLSFGLYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNIGCSDLLLTVSLP MDLPPQLSFGLYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCSDLLLTVSLP н 셤 ઠે

120 61 LKAVEALASGAWPLPASLCPVPAVAHFPPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRP ઠે ద

180 CYSWGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAWDPASAG 121 ઠે a

240 240 PARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHRRKKLRAAWVAGGALLTLLLCVGPY PARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGGALLTLLLCVGPY 181 181 ठ 셤

8 8

241 NASNVASFLYPNIGGSWRKLGLITGAWSVVLNPLVTGYLGRGPGLKTVCAARTQGGKSQK 300

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95; Conservative
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Best Local Similarity
Matches 95; Conserv
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Best Local Si
Matches 93;
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C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Date: 03-Dec-1997 #sequence_revision 03-Dec-1997 #text_change 29-Sep-1999
A.Title: December: 02-Sep-1995
A.Title: 03-Dec-1997 #sequence_revision 03-Dec-1997 #text_compled receptor 03-Manager 03-Manag
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JUESTIE

G protesin-coupled receptor 41 - human

C;Species Man Sapiens (man)

C;Date: 03-Dec-1997 #sequence_revision 03-Dec-1997 #text_change 29-Sep-1999

C;Accession: JC5715

R;Sawadargo, M; George S.R.; Nguyen, T.; Xu, S.; Kolakowski Jr., L.F.; O'Dowd, B.F.

Biochem. Biophys. Res. Commun. 239, 543-547, 1997

A;Title: A cluster of four novel human G protein-coupled receptor genes occurring in clc

A;Reference number: JC5714, MUID:98008875; PMID:9344866

A;Accession: JC5715

A;Accession: JC5715

A;Molecule type: MRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DILLITVSLPLKAVEALASGAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFP 111
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A,Cross-references: GB:AF024688; NID:g2612947; PIDN:AAB86711.1; PID:g2612948
C,Superfamily: G protein-coupled receptor 43
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Pred. No. 3e-23;
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34.1%;
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Best Local Similarity
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Grotein-coupled receptor 43 - human
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: O3-Dec-1997 #sequence_revision O3-Dec-1997 #text_change 29-Sep-1999
C.Accession: JC5717
R.Sawadargo, M.; George, S.R.; Nguyen, T.; Xu, S.; Kolakowski Jr., L.F.; O'Dowd, B.F.
B.Schem. Blophys. Res. Commun. 239, 543-547, 1993
A.Title: A cluster of four novel human G protein-coupled receptor genes occurring in clost A.Reference number: JC5717
A.A.A.Cession: JC5717
A.A.A.Cession: JC5717
A.Reference number: JC5717
A.Refere
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DILLITVSLPLKAVBALASGAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFP 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            172 EAW---DPASAGPARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGG 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 YVAAFALGFPLNVLAIRGATAHARL-RLTPSLVYALNLGCSDLLLTVSLPLKAVEALASG
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F;128-147/Domain: transmembrane #status predicted <TM4>
F;128-204/Domain: transmembrane #status predicted <TM5>
F;20-242/Domain: transmembrane #status predicted <TM6>
F;250-276/Domain: transmembrane #status predicted <TM6>
F;256-276/Domain: transmembrane #status predicted <TM7>
F;151,167/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           229 ALLTLLLCVGPYNASNVASFLYPNLGGSWRKLGLITGAWSVVLNPLVTGYLGRG
                                                                                                                                                                                                                                                                                                                                                                                                                    24;
F;229-250/Domain: transmembrane #status predicted <TW6>
$1.559-278/Domain: transmembrane #status predicted <TW7-
F;166/Binding site: carbohydrate #status predicted
F;295/Binding site: palmitate (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                    41; Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                21.9%; Score 347; DB 2; 32.3%; Pred. No. 1.2e-21;
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C)Accession: S1748
R)Rammssen, U.B.; Vouret-Craviari, V.; Jallat, S.; Schlesinger, Y.; Pages, G.; Pavirani, PEBS Lett. 288, 123-128, 1991
A;Title: cDNA cloning and expression of a hamster alpha-thrombin receptor coupled to Ca(; A;Reference number: S17148; MUID:91348247; PMID:1652467
                                                                                                                                                   269 YYFSA-----FSAVFFFVPLIISTVCYVSIIRCLSSSAVANRSKKSRALFLSAAVFCIF 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            227 WALAIA--GVVPLVLKEQTIQVPG------LNITT-----CHDVLNETLLEGYYA 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178 ---SAGPARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHR-RKLRAAWVAGGALLTL 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169 DWQFGSGMCRFATAAFYCNMYASIMLMTVISIDRFLAVVYPIQSLSWRTLGRANFTCLVI 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          229 WVWAI--MGVVPLLLKEQTTRVPG-----LNITT-----CHDVLNETLLQGFYS 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---SAGPARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHR-RKLRAAWVAGGALLTL 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               271 YYFSA-----FSAVFFLVPLIISTICYMSIIRCLSSSSVANRSKKSRALFLSAAVFCVF 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Solution teceptor 5 - rat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alpha-thrombin receptor - Chinese hamster
C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
                                                                                                  11 LYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCSDLLLTVSLPLKAVEALASG
                                                                                                                                                                                                                                                                                                                                 167 DWQFGSBLCRFVTAAFYCNMYASILIMTVISIDRFLAVVYPMQSLSWRTLGRASFTCLAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131 WALVLCHIGLV-----FGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAWDPA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 LYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCSDLLLTVSLPLKAVEALASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 AWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRPCYSWGVCAAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131 WALVLCHIGLVFGL-----EAPGGWLDHSNTSLGINTPVNGSPVCLEAWDPA----
                                                                                                                                                                                                                                                                  71 AWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRPCYSWGVCAAI
                 42; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X61958; NID:g940495; PIDN:CAA43957.1; PID:g49538
C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 427;
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13.4%; Score 213; DB 2; Length 42°
Best Local Similarity 23.4%; Pred. No. 2.4e-10;
Matches 68; Conservative 53; Mismatches 122; Indels
                 46; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      234 LLCVGPYNASNVASFLY 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                323 IICFGPTNVLLIAHYSF 339
             65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-427 < RAS>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cipemoin Inceptual Antican clawed frog)
Cipemoin Inceptual Cartican clawed frog)
Cipede: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
Cipede: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
Cipede: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
Cipedezten, R.E.; Chen, J.; Ishii, M.; Ishii, K.; Nanevicz, T.; Turck, C.W.; Vu, T.H.; C
Nature 368, 648-651, 1994
NyTitle: Thrombin receptor's specificity for agonist peptide is determined by its extract
A;Reference number: IS1667; MUID:94195429; PMID:8145852
A;Accession: IS1667
A;Accession: IS1667
A;Accession: L51667
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-420 cGER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rivu, T.K.H.; Hung, D.T.; Wheaton, V.I.; Coughlin, S.R.
Cell 64, 1057-1068, 1991
A;Title: Molecular cloning of a functional thrombin receptor reveals a novel proteolytic
A;Reference number: A37912, MUID:91168254; PMID:1672265
A;Accession: A37912
A;Molecule type: mRNA
A;Residues: 1-425 <VUA>
182 ELCLVLPPIPMAVTIFCYWRFVWIMLSQPLVGAQRRR--RAVGLAVVTLLNPLVCFGPYN 239
                                                                                                                                          295
                                                                                                                                                                                      240 VSHLVGY-HQRKSPWWRSIAVVPSSLNASLDPLLPYFSSSVVRRAFGRGLQVL---RNQG 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LYTVVFIVGLPINLLAIIIFLFRWRVR-KPAVVYMLNLAIADVFFVSVLPFKIAYHLSGN 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    166 DWLFGPGMCRIVTAIFYCNMYCSVLLIASISVDRFLAVVYPMHSLSWRTWSRAYMACSF1 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71 AWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRPCYSWGVCAAI 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             185 ---SLSLLLFFLPLAITAFCYVGCLRALARSGLTHR-RKLRAAWVAGGALLTLLLCVGPY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131 WALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSP-----VCLEAWDPASAGPARF- 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        226 WLISIA-------STIPLLVTEQTQKIPRLDITTCHDVLDLKDLKDFYIY 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         269 YFSSPCLLFFFVPFIITICYIGIIRSLSSSSIENSCKKTRALFLAVVLCVFIICFGPT 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 LYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCSDLLLTVSLPLKAVEALASG 70
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A;Map position: 5q13-5q13
C;Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
E;1-26/Domain: signal sequence #status predicted <SIG>
F;27-425/Product: thrombin receptor #status predicted <MAT>
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C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 05-Nov-1999
                                                                                                                                     242 ASNVASFLYPNIGGSWRKIGLITGAWSVVINPLVTGYLGR-----GPGLKTVCAARTQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:U09632; NID:g495197; PIDN:AAA18498.1; PID:g495198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 N-----ASNVASFLYPNLGGSWRKIGLITGAWSVVLNPLVTGY 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 420;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.4%; Score 41., 25.0%; Pred. No. 6e-13;
tive 44; Mismatches 126; Indels
                                                                                                                                                                                                                                                                                                                                              RESULT 5
151667
thrombin receptor - African clawed frog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 25.0 Matches 72; Conservative
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Best Local Si
Matches 63;
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Best Local S
Matches 83
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JULET-BOUKIN-8 receptor - rabbit
Interleukin-8 receptor - rabbit
Interleukin-8 receptor - rabbit
C.Species: Oryctolagus cuniculus (domestic rabbit)
C.Species: Oryctolagus cuniculus (domestic rabbit)
C.Species: J1-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 05-Nov-1999
C.Accession: J01231; A46483
R.Beckmann, M.P.; Munger, W.E.; Kozlosky, C.; VandenBos, T.; Price, V.; Lyman, S.; Gerar Blochem: Blochem: Blochem: J01231; MulD:91378994; PMID:1898400
A;Accession: J01231
A;Title: Molecular characterization of the interleukin-8 receptor.
A;Reference number: J01231; MulD:91378994; PMID:1898400
A;Accession: J01231
A;Hillecule type: DNA
A;Nesidues: 1-355 <-BEC>
A;Cross-references: GB:M74240; NID:9165438; PIDN:AAA31375.1; PID:9165439
                                                                                                                                       A;Residues: 1-363 <OCA1>
A;Cross-references: GB:L04535; NID:g409238; PIDN:AAA17029.1; PID:g409239
R;O'Carroll, A.M.; Lolait, S.J.; Konig, M.; Mahan, L.C.
Mol. Pharmacol. 44, 1278, 1993
A;Title: Maccular cloning and expression of a pituitary somatostatin receptor with pref A;Reference number: IS7949; MUID:94088493; PMID:8264565
A;Title: Molecular cloning and expression of a pituitary somatostatin receptor with pref
A;Reference number: 157940; MUID:93125499; PMID:1362243
A;Accession: 157940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 AWPLPASLCPVF----AVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRPCYSWGV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          102 YWPPGSFLCRLVMTLDGINQFTSIFC----LMVMSVDRYLAVVHPLRSARWRRPRVAKWA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              158 SAAVWVFSLLMSLPLLVFADVQEGW--------GTCNLSWPEPVGLWGAAF 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201 ITYTSVLGFFGPLLVICLCYLLIVVKVKAAGMRVGSSRRRRSEPKVTRMVVVVLVFVGC 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --PYNASNVASFLY----PNLGGSWRKLGLITGAWSVVLNPLVTGYLG---RGPGLKTV 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           261 WLPFFIVNIVNLAFTLPEEPTSAGLYFFVVVLSYANSCA-NPLLYGFLSDNFRQSFRKVL 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAAIWAL-VLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAW-DPASAGPARF 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;MOJECULE type: mRNA
A;Residues: 309-363 <PEN>
A;Cross-references: EMBL:X74828; NID:g433911; PIDN:CAA52825.1; PID:g433912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --SISILLFFLPLAITAFCYVGCLRALARSGL---THRRKLRAAWVAGGALLTLLLCVG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 LYVAAFALGPPLNVLAIRGATAHARLRLTPSLVYALNLGCSDLLLTVSLPLKAVEALASG
                                                                                                                                                                                                                                                                                                         A,Accession: 157949
A,Accession: 157949
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: all-163 ACCA2>
A;Residues: 341-363 ACCA2>
A;Residues: 341-363 ACCA2>
A;Cross-references: GB:867370; NID:g455947; PIDN:AAB29371.1; PID:g455948
A;Experimental acurce: pituitary
R;Penetta, R; Greenwood, M.; Patel, Y.C.
R;Penetta, R.; Greenwood, M.; Patel, Y.C.
A;Penetta, R.; Greenwood, M.; Patel, Y.C.
A;Penetta, R.; Greenwood, M.; Patel, Y.C.
A;Penetta, R.; Greenwood, M.; Patel, Y.C.
A;Reference number: S39244
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                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Gene: SSTR5
C, Superfamily: vertebrate rhodopsin
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C'Accession: A43448

Z. R. Z. R. S. Z. C., Fayzer, D. J., Corson, M.A.; Runge, M.S.
J. Biol. Chem. 267, 16975-16979, 1992

A, Title: Molecular cloning of the rat vascular smooth muscle thrombin receptor. Evidence A, Title: Molecular and A448; MUID:92381002; PMID:1324917

A, Reference number: A43448; MUID:92381002; PMID:1324917

A, Status: preliminary
RiLee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.
J. Immunol. 148, 1261-1264, 1992
J. Immunol. 148, 1261-1264, 1992
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A.Title: Characterization of complementary DNA clones encoding the rabbit IL-8 receptor. A; Reference number: A46483; MUID:92148149; PMID:1737938
A; Recession: A46483
A; Recession: preliminary
A; Molecule type: mRNA
A; Residues: 1-355 < LEE>
A; Cross-references: GB: M82873; NID:g165440; PIDN:AAA31376.1; PID:g165441
A; Residues: aneutrophils
A; Reperimental source: neutrophils
A; Note: sequence extracted from NCBI backbone (NCBIN:81526, NCBIP:81530)
C; Superiamlly: vertebrate rhodopsin
C; Keywords: G protein-coupled receptor; transmembrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48 VVIYALVFLISLGNSLVMLVILYSRSNRSVTDVYLLNLAMADLLFALTMPIWAVS--KE 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    165 IWALSLI-LSLPFFLFRQ------VFSPNNSSPVC---YEDLGHNTAKWRWVLR 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----ASNVASFLYPNLGGSWRKLGLITGAWSVVLN 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRPCYSWGVCAA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106 KGWIFGTPLCKVVSLVKEVNPYSGILLLACISVDRYLAIVHATRTLTQKRHLVKF-ICLG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 IWALVICHIGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAWDPASAGPARFSLSLL 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            190 L-----FFLPLAITAFCYVGCLRAL--ARSGLTHRRKLRAAWVAGGALLTLLLCVGPYN 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                209 ILPHTEGFILPLIVMLFCYGFTLRTLFQAHMGOKH----RAMRVIFAVVLIFLLCWLPYN 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----CLN 306
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 VAAFALGFPLNVLA---IRGATAHARLRLTPSLVYALNLGCSDLLLTVSLPLKAVEALAS
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A;Experimental source: RASM aortic smooth muscle cells
A;Note: sequence extracted from NCBI backbone (NCBIN:111973, NCBIP:111974)
C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 LYVAAFALGFPLNVLAIRGATAHARLRL-TPSLVYALNLGCSDLLLTVSLPLKAVEALAS
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24.5%; Pred. No. 1.4e-09;
tive 46; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 12.9%; Score 204.5; DB 2; Length . 1 Similarity 25.8%; Pred. No. 1e-09; 83; Conservative 39; Mismatches 117; Indels
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Discipled P2 receptor - rat
Clispecies: Rattus norvegicus (Norway rat)
Clispecies: Rattus norvegicus (Norway rat)
Clispecies: Rattus norvegicus (Norway rat)
Clispecies: O2-U11-1996 #sequence_revision 02-U11-1996 #text_change 19-May-2000
Clispecies: O2-U11-1996 #sequence_revision 02-U11-1996 #text_change 19-May-2000
Clispecies: O2-U1-1996 #sequence_revision 02-U11-1996 #text_change 19-May-2000
Clispecies: CS-S152-S26158, 1995
A.F. Chang, K.; Kumada, M.; Takuwa, Y.
A.F. Ference number: 155450; MUID: 96064682; PMID: 7592819
A.F. A.F. Changeris of an ovel P2 nucleotide receptor.
A.F. A.F. Changeris of a novel P2 nucleotide receptor
A.F. A.F. Changeris of an ovel P2 nucleotide receptor
A.F. Changeris of B1051665; NID: 91066007; PIDN: BAA09816.1; PID: 91066008
C. Superfamily: ATP receptor P2u
C. Keywords: G protein-coupled receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 AVEALASGAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLG---YQAFRR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 PCYSWGVCAAIWALVL--CHLGLVPGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAWDPA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178 SAG---PARFSLSLLLFFLPLAITAFCYVGCLRA--LARSG-----LTHRRKLRAAWVAG 227
                                                                                                                                                                                                           A;Reference number: H01373
A;Accession: G02514
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 'M', 4-328 <HAM>
A;Cross-treferences: EMBL:U52464; NID:g1407632; PIDN:AAB03572.1; PID:g1407633
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29 LPP----VYSAVLAAGLPLNICVIT-QICTSRRALTRTAVYTLNLALADLLYACSLPLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 LPPQLSFGLYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCSDLLLTVSLPLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        228 GALLTLLLCVGPYNASNVASFLYPNLGGSWRKLGLITGAWSVVLNPLVTGYLGRGP 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;104-122/Domain: transmembrane #status predicted <TVM3>
F;14-167/Domain: transmembrane #status predicted <TVM4>
F;143-216/Domain: transmembrane #status predicted <TVM5>
F;241-264/Domain: transmembrane #status predicted <TVM6>
F;283-305/Domain: transmembrane #status predicted <TVM7>
F;283-305/Domain: transmembrane #status predicted <TVM7>
F;5,173/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Keywords: glycoprotein; placenta; receptor; transmembrane protein F;26-52/Domain: transmembrane #status predicted <TWM1> F;63-86/Domain: transmembrane #status predicted <TWM2>
A.Cross-references: EMBL:X97058
A.Experimental source: placenta
R.Hammet, F.; Southey, M.C.; Somers, G.R.; Hutchins, A.M.; Venter,
submitted to the EMBL Data Library, March 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: P2Y6
C;Superfamily: ATP receptor P2u
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            interleukin-8 receptor (clone 5Bla) - rabbit (Species: Oryctolagus cuniculus (domestic rabbit) (Species: Oryctolagus cuniculus (domestic rabbit) (Species: Oryctolagus cuniculus (domestic rabbit) (Species: Or-Van-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999 (Spacesion: A53752 R.P. Thomas, K.M.; Suzuki, H.; LaRosa, G.J.; Wilkinson, N.; Folco, E.; Navarro J. Biol. Chem. 269, 12391-12394, 1994 (Appl. 1200) (Appl. 1200)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Communi, D.; Parmentier, M.; Boeynaems, J.M.
Biochem. Biophys. Res. Commun. 222, 303-308, 1996
A;Title: Cloning, functional expression and tissue distribution of the human P2Y6 recept
A;Reference number: JC4800; MUID:96222498; PMID:8670200
A;Accession: JC4800
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                        275 SYYFSA-----PSAIPPLVPLIISTVCYTSIIRCLSSSAVANRSKKSRALFLSAAVFCI 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187 ---PPNSSPVCYEDMGNSTA-KWRWVLRILPQTFGFILPLLVMLFCYVFTLRTLFQAHMG 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LINIGCSDILLITVSLPLKAVEALASGAWPLPASILCPVFAVAHFFPLYAGGGFLAALSAGRY 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106 LGAAFPLGYQAFRRP----CYS-WGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLG 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144 LAIVHATRIMIQKRHLVKFICLSMWGVSLILSLPILLFRNAIF-------- 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 DLPPTLLDSAPCRSESLETNSYVVLITYILVFLLSLIGNSLVMLVILYSRSTCSVTDVYL 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DLPP------QLSFGLYVA--AFALGPPLNVLA---IRGATAHARLRLTPSLVYA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Species: Homo sapiens (man)
Date: 15-Oct-1995 #sequence_revision 16-Aug-1996 #text_change 17-Nov-2000
Accession: JC4800; G02514
                                                                                                   233 IWVMAI--MGVVPLLLKEQTTQVPG-----LNITT-----CHDVLNETLLHGFY
                                                                                                                                                                                                           ---SAGPARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHR-RKLRAAWVAGGALLT
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IWALVICHLGLVFGL-----EAPGGWLDHSNTSLGINTPVNGSPVCLEAWDPA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
12.7%; Score 201; DB 2; Length 358;
Best Local Similarity 25.5%; Pred. No. 2e-09;
Matches 89; Conservative 34; Mismatches 122; Indels 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           245 VASFLYPNLGGSWRKLGLITGAWSVVLNPLVTGYLGR--GPGLKTVCAA 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   299 ILGFLHS------CLNPIIYAFIGOKFRYGLLKILAA 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214 LTHRRKLRAAWVAGGALLTLLLCVGPYN------
                                                                                                                                                                                                                                                                                                                                                                                                                       233 LLLCVGPYNASNVASFL 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          329 PIVCFGPTNVLLIVHYL 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-358 <PRA>
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JC4800
P2Y6 receptor - human
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12;

51; Gaps

82

10; 62 3 LPPQLSFGLYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCSDLLLTVSLPLK Gaps 47; Length 328; Indels Query Match
12.5%; Score 197.5; DB 2;
Best Local Similarity 26.2%; Pred. No. 3.7e-09;
Matches 77; Conservative 30; Mismatches 140;

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A;Cross-references: EMBL:X65858; NID:g312046; PIDN:CAA46688.1; PID:g312047
R;Ahuja, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.
J. Biol. Chem. 269, 26381-26389, 1994
A;Title: Comparison of the genomic organization and promoter function for human interleub
A;Reference number: 137898; MUID:95014476; PMID:7929358
                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-350 <RE2>
A; Accession: 138 0 <RE2>
A; Accession: 138711
A; Molecule type: mRNA
A; Accession: 138711
A; Molecule type: mRNA
A; Residues: 1-16 <RE3>
A; Cross: references: EMBL:U11871; NID:9511806; PIDN:AAA64379.1; PID:9733002
A; Residues: 1-16 <RE3>
A; Cross: references: EMBL:U11871; NID:9511806; PIDN:AAA64379.1; PID:9733002
B; Holmes, W.E.; Lee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.
Science 253, 1278-1280, 1991
A; Reference number: A39445; MUID:91369199; PMID:1840701
A; Reference number: A39445
A; Molecule type: mRNA
A; Residues: 1-275, TY, 277-350 <HOL>
A; Residues: 1-275, TY, 277-350 <HOL>
A; Cross: references: GB:M68932; NID:9186369; PIDN:AAA59159.1; PID:9186370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 NGWIFCTFLCKVVSLLKEVNFYSGILLLACISVDRYLAIVHATRTLTQKRHLVKF-VCLG 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L----FFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGGALLTLLLCVGPYNASNV 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          206 PHTEGFIVPLEVMLFCYGFTLRTLFKAHM--GQKHRAMRVIFAVVLIFLLCWLPYNLVLL 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130 IWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAWDPASAGPARFSLSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 VAAFALGFPLNVLA---IRGATAHARLRLTPSLVYALNLGCSDLLLTVSLPLKAVEALAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Cross-references: GDB:135039, OMIN:146929
A,Map position: 243-2435
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein, membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             264 ADTLMRTQVIQESCERRNNIG---RALDATEILGFLHSCLNPIIYAFIGQ 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               246 ASFLY------PNLGGSWRKLGL--ITGAWSVVLNPLVTGYLGR 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.3%; Score 194.5; DB 2; 28.3%; Pred. No. 7e-09; tive 39; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: April 29, 2004, 12:12:04 Job time : 22 secs
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nes 82, Conservative
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Best Local Si
Matches 82;
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NyAlternate names: interleukin-8 receptor, high-affinity
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence revision 12-Apr-1996 #text_change 05-Nov-1999
C;Accession: 137449; 138710; 138711; A39445
R;Mollereau, C; Muscatelli, F; Mattei, M.G.; Vassart, G.; Parmentier, M.
Genomics 16, 248-251, 1993
A;Title: The high-affinity interleukin 8 receptor gene (IL8RA) maps to the 2q33-q36 regi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               re
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PEBS Lett. 375, 121-124, 1995

A;Title: Cloning, sequencing and tissue distribution of two related G protein-coupled A;Ference number: S68207; MUID:96087098; PMID:7498459
A;Accession: S68207
A;Status: preliminary; nucleic acid sequence not shown
                                                                            63 AVEALASGAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLG----YQAFRR 119
                                                                                                                                                                                                                                             120 PCYSWGVCAAIWALVL--CHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAWDPA 177
                                                                                                                                                                                                                                                                                                                                                                                                         178 SAG---PARFSISILIFFIPLAITAFCYVGCLRALARSG----LITHRRKLRAAWVAGGA 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                            75 DYFLHHDNWIHGPGSCKLRGFIFYTNIYISIAFLCCISVDRYLAVAHPLRFARLRRVKTA 134
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                                                                                                                                                                                                                                                                                                                     -----AATGIQ---RNRTVCYDLSPPI 184
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A,Gross-references: BMBL:U35399; NID:g1015420; PIDN:AAA79061.1; PID:g1015421
C,Superfamily: G protein-coupled receptor 4
C;Keywords: G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G protein-coupled receptor 6C.1 - human
C;Species: Homo sapiens (man)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 29-Sep-1999
C;Accession: S68207
29 LPP-----VYSVVLVVGLPLNVCVIAQICA-SRRTLTRSAVYTLNLALADLLYACSLPLL
                                                                                                                               4 PPQLSFGLYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNIGCSDLLLTVSLPLKA
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Best Local Similarity 27.2%; Pred. No. 5.9e-09;
Matches 74; Conservative 30; Mismatches 115; Indels 53
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                                                                                                                                                                                                                                                                                               143 A--AWVVCGVVWLVVTAQCLPTAVF----
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11;

43;

Length 350; Indels

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GenCore version 5.1.6
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April 29, 2004, 12:11:34 ; Search time 47 Seconds (without alignments) 1769.295 Million cell updates/sec OM protein - protein search, using sw model Run on:

US-10-202-687-2 Title: Perfect score:

1 MDLPPQLSFGLYVAAFALGF.....RGPGLKTVCAARTQGGKSQK 300 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1138120 Total number of hits satisfying chosen parameters: 1138120 seqs, 277189581 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published_Applications_AA:* Database

'(cgn2_6/ptodata/2/pubpaa/USO7_PUBCCMB.ppp:*
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'(cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.ppp:*) /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	250, App	475, App	33080, A	2, Appli	272, App	4, Appli	254, App	605, App	2, Appli	33898, A	274, App	2, Appli			467, App
Description	Sequence 250,	Sequence 475,	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence 605	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
ΙD	US-10-251-385-250	US-10-225-567A-475	US-10-029-386-33080	US-10-202-687-2	US-10-251-385-272	US-10-203-539-4	US-10-251-385-254	US-10-225-567A-605	US-10-203-539-2	US-10-029-386-33898	US-10-251-385-274	US-10-348-190-2	US-10-348-190-4	US-10-251-385-258	US-10-225-567A-467
DB	14	14	14	15	14	14	14	14	14	14	14	14	14	14	14
* Query Match Length DB	300	300	300	300	300	346	346	346	346	401	346	330	330	330	330
& Query Match	100.0	100.0	100.0	100.0	99.7	23.1	21.9	21.9	21.9	21.9	21.6	21.5	21.1	21.0	21.0
Score	1584	1584	1584	1584	1579	366	347	347	347	347	342	340.5	334	332	332
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22, 24, 25, 27, 27, 27, 27, 27, 27, 27, 27, 27, 27	Sequence 149, App Sequence 2, Appli Sequence 76, Appl Sequence 2, Appli
14 US-10-337-992-2 14 US-10-029-886-34068 1 US-09-853-161-104 9 US-09-853-161-104 12 US-10-058-39-104 14 US-10-058-39-104 15 US-09-852-69A-104 16 US-10-081-810-41 17 US-10-081-810-41 18 US-10-081-810-41 19 US-10-081-810-42 10 US-09-782-980-80 10 US-09-782-980-80 10 US-09-782-980-80 10 US-09-782-980-80 10 US-09-782-980-80 10 US-09-782-980-80 10 US-10-187-049-2 11 US-11-17-293-13 12 US-11-17-293-13 13 US-11-17-293-13 14 US-11-17-293-13 15 US-11-17-293-13 16 US-11-18-186-186 17 US-11-190-469-1	15 US-10-417-820A-149 9 US-09-739-151-2 10 US-09-782-974C-76 12 US-10-081-810-2
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332 332 332 332 332 332 332 332 332 332	222.5 221.5 221.5 221.5
0 1 1 1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	4 4 4 4 2 6 4 3

ALIGNMENTS

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Sequence 250, Application US/10251385
| Publication No. US20030105292A1
| GENERAL INFORMATION:
| APPLICANT: Behan, Dominic P. |
| APPLICANT: Chalmers, Derek T. |
| APPLICANT: Liaw, Chen W. |
| TITLE OF INVENTION: Receptors |
| TITLE OF INVENTION: Receptors |
| FILE REFERENCE: AREN-0040 |
| CURRENT APPLICATION NUMBER: US/10/251,385 |
| CURRENT FILING DATE: 1998-10-13 |
| NUMBER OF SEQ ID NOS: 294 |
| SEQ ID NO 250 |
| SEQ ID NO 250 |
| LENGTH: 300 |
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| LENGTH: 300 |
| CONSTRUCTOR APPLICATION NUMBER: Without the second of the sec
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Best Local Similarity 100.
Matches 300; Conservative
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; ORGANISM: Homo sapiens
US-10-251-385-250
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61 LKAVEALASGAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRP 120

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121 CYSWGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAWDPASAG 180

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61 LKAVEALASGAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRP 120
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APPLICANT: OLDE, BJORN
APPLICANT: OLDE, BJORN
APPLICANT: OLDE, BJORN
APPLICANT: NICLAS
APPLICANT: NICLAS
APPLICANT: NICLAS
APPLICANT: NICLAS
APPLICANT: FLODSREN, BRIK
TITLE OF INVENTION: METABOLISM
FILE REFERENCE: 07675.0007 SEQUENCE LISTING
CURRENT FILING DATE: 2002-07-24
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                       Length 300;
               SEQ ID NO 33080

LENGTH: 300

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: MAP TO U62631.1

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.89

OTHER INFORMATION: WISSPROT HIT: O14842, EVALUE 0.00e+00

US-10-029-386-33080
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100.0%; Score 1584; DB 14;
Best Local Similarity 100.0%; Pred. No. 4.4e-139;
Matches 300; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 1584; DB 15; Best Local Similarity 100.0%; Pred. No. 4.4e-139; Matches 300; Conservative 0; Mismatches 0;
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/10202687
Publication No. US20040019109A1
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ORGANISM: Homo sapiens
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LENGIH: 300
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Publication No. US20030113798A1

Publication No. US20030113798A1

Publication No. US20030113798A1

APPLICANT: InfoRMATION:
APPLICANT: Brown, Joseph P.
APPLICANT: Brown, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS FILE REFERENCE: 1220-4-4

CURRENT APPLICATION NUMBER: US/10/225,567A

CURRENT FILING DATE: 2000-12-19

PRIOR PILING DATE: 2000-12-19

NUMBER OF SEQ ID NOS: 2292

SOFTWARE: Patentin version 3.1
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Publication No. US20030194704A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Penn, Barid K.

APPLICANT: Hanzel, David K.

APPLICANT: APPLICATION NUMBER: US/10/029,386

CURRENT APPLICATION NUMBER: US/10/12-20

NUMBER OF SEQ ID NOS: 34288
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                                                                                                                                                                                241 NASNVASFLYPNLGGSWRKLGLITGAWSVVLNPLVTGYLGRGPGLKTVCAARTQGGKSQK 300
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  121 CYSWGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAWDPASAG 180
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                                                                                    PARFSLSLILFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGGALLTLLLCVGPY
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                                                    PARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGGALLTLLLCVGPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 300; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-475
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Best Local Similarity
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US-10-029-386-33080
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US-10-225-567A-475
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APPLICANT: Behan, Dominic P.
APPLICANT: Behan, Dominic P.
APPLICANT: Lidaw, Chen W.
TITLE OF INVENTION: Receptors
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
CURRENT FILING DATE: 2002-09-20
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: PATENTIN VERSION 3.1
LENGTH: 1346
LENGTH: 346
LENGTH: 346
LENGTH: 346
LENGTH: 346
LENGTH: 346
LENGTH: 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 LGYQAPRRPCYSWGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVC- 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229 ALLTLLLCVGPYNASNVASFLYPNLGGS--WRKLGLITGAWSVVLNPLVTGYLGRG 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28; Gaps
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23.1%; Score 366; DB 14; 1
Best Local Similarity 34.1%; Pred. No. 1.1e-25;
Matches 101; Conservative 38; Mismatches 129;
PRIOR APPLICATION NUMBER: GB 0007015.1
PRIOR FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 12
SOPTWARE: PATENTIN VET. 3.0
SEQ ID NO 4
LENGTH: 346
TYPE: PRT
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 254, Application US/10251385 Publication No. US20030105292A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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Publication No. US20030105292A1
GRNERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. US20030105292A1-Endogenous, Constitutively Activated Human (TITLE OF INVENTION: Receptors FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/10/251,385
CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: US/09/170,496
PRIOR PILING DATE: 1998-10-13
240
                                                                                                                       PARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGGALLTLLLCVGPY 240
                                                                                                                                                                                                                                                                      241 NASNVASFLYPNIGGSWRKIGLITGAWSVVINPLVTGYLGRGPGIKTVCAARTQGGKSQK 300
                                                                                                                                                                                                                                                                                                                 241 NASNVASPLYPNLGGSWRKLGLITGAMSVVLNPLVTGYLGRGPGLKTVCAARTQGGKSQK 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 LKAVEALASGAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 PARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGGALLTLLLCVGPY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 NASNVASFLYPNIGGSWRKIGLITGAWSVVINPLVTGYLGRGPGLKTVCAARTQGGKSQK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 NASNVASFLYPNLGGSWRKLGLITGAWSVVLNPLVTGYLGRGPGLKTVCAARTQGGKSQK 300
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                                                                                                                                                                  181 PARFSLSLLLFFLFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWYAGGALLTLLLLCVGPY
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Publication No. US20030113810A1
GENERAL INFORMATION:
APPLICANT: GLAXO GROUP LIMITED
TITLE OF INVENTION: NOVEL ASSAY
FILE REFERENCE: PG3849USw
CURRENT APPLICATION NUMBER: US/10/203,539
CURRENT FILING DATE: 2002-08-09
FRIOR APPLICATION NUMBER: GB 0003900.8
PRIOR FILING DATE: 2000-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 294
SOFWHARB: Patentin version 3.1
SEQ ID NO 272
LENGTH: 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-251-385-272
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Sequence 33898, Application US/10029386

; Sequence 33899, Application US/10029386
; Publication No. US20030194704A1
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David R.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USFFUL FOR GI
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: ACONICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT APPLICATION NUMBER: US/10/029,386
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 33898
; SEQ ID NO 33898
; ENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 DILLILFEPERMYEAANGMHWPLPPILCPISGFIFFTIYITALFLAAVSIERFESVAHP 120
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NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 3.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95; Conservative
                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (229) .. (250)
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; LOCATION: (259)..(278)
US-10-203-539-2
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Best Local Similarity
Matches 95; Conserv?
                                                                                                                                                                               LOCATION: (18)..(41)
                                                                                                                                                                                                                                             (52) .. (73)
                                                                                                                                   FEATURE:
NAME/KEY: TRANSMEM
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LOCATION:
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APPLICANT: Brown, Joseph P.
APPLICANT: Brown, Joseph P.
APPLICANT: Brown, Joseph P.
APPLICANT: Brumer, Gaena C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REPERBURE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR APPLICATION NUMBER: 60/257,144
NUMBER OF ESQ ID NOS: 2292
SOFTWARE: Patentin version 3.1
  121 LWYKTRPRLGQAGLVSVACWLLASAHCSVVYVIEFSGD-ISHSQGTNG------TCY 170
                                              172 EAW---DPASAGPARFSLSLILFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGG 228
                                                                       61 DLLLLFLPRRWVEAANGMHWPLPFILCPLSGFIFFTTIYLTALFLAAVSIERFLSVAHP 120
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                                                                                                                                                            230 TLLNFLVCFGPYNVSHVVGYICGE-SPAWRIYVTLLSTLNSCVDPFVYYFSSSG 282
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                                                                                                                                     229 ALLTILLCVGPYNASNVASFLYPNLGGSWRKLGLITGAWSVVLNPLVTGYLGRG 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Sequence 2, Application US/10203539 | Publication No. US20030113810A1 |
| GENERAL INFORMATION: ILMITED |
| TITLE OF INVENTION: NOVEL ASSAY |
| FILE REFERENCE: PG3849USw |
| CURRENT APPLICATION NUMBER: US/10/203,539 |
| CURRENT FILING DATE: 2002-08-09 |
| PRIOR APPLICATION NUMBER: GB 0003900.8 |
| PRIOR PILING DATE: 2000-02-18 |
| PRIOR PILING DATE: 2000-02-18 |
| PRIOR FILING DATE: 2000-03-22 |
                                                                                                                                                                                                                                                                                       Sequence 605, Application US/10225567A Publication No. US20030113798A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-605
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LENGTH: 346
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US-10-203-539-2
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APPLICANT: Loudhed, Jamila
APPLICANT: Loudhed, Jamila
APPLICANT: Loudhed, Jamila
APPLICANT: Loudhed, Jamila
APPLICANT: Levitt, Roy
APPLICANT: Diological Levitt, Roy
APPLICANT: Dong, Qu
TITLE OF INVENTION: Atchima Associated Factors as Targets for Treating
TITLE OF INVENTION: Atchima Associated Factors as Targets for Treating
TITLE OF INVENTION: Atchima Associated Factors as Targets for Treating
TITLE OF INVENTION: Atchima Associated Factors as Targets for Treating
TITLE OF INVENTION: Atchima Associated Factors as Targets for Treating
FILE REFERENCE: 036870-5072
CURRENT APPLICATION NUMBER: US/09/157,24
FRIOR FILING DATE: LARLIER PAPLICATION NUMBER: 60/059,510
FRIOR PILING DATE: EARLIER FILING DATE: 1996-12-02
FRIOR FILING DATE: EARLIER FILING DATE: 1996-12-02
SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
SEQ ID NOS: 2
LENGTH: 330
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171 LEFRKDQLAILLPVRLEMAVVLFVVPLIITSYCYSRLVWILGRGG-SHRRQRRVKGLLAA 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 SHLVGF-YLRQSPSWRVEAVVFSSLNASLDPLLFYFSSSVVRRAFGKGLLLIRNPASSML 299
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                                                                               230 TLINFLVCFGPYNVSHVVGYICGE-SPAMRIYVTLLSTLNSCVDPFVYYFSSSG 282
                                                     229 ALLTLLLCVGPYNASNVASFLYPNLGGSWRKLGLITGAWSVVLNPLVTGYLGRG 282
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Publication No. US20030166150A1
GENERAL INFORMATION:
APPLICANT: Renauld, Jean-Christophe
APPLICANT: Louahed, Jamila
APPLICANT: Levitt, Roy
                                                                                                                                                                                                                                                                                                                             Jean-Christophe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    280 GRGPGLKTVCAARTQGGKSQ 299
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Publication No. US20030166150A1
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Matches 99; Conservative
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; ORGANISM: Murinae gen. sp
US-10-348-190-2
                                                                                                                                                                                                                                                                                                GENERAL INFORMATION: APPLICANT: Renauld,
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US-10-348-190-4
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Sequence 274, Application US/10251385
Publication No. US20030105292A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: Proctein-Coupled
TITLE OF INVENTION: Receptors
FILE REFREENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/10/251,385
CURRENT PILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: US/09/170,496
PRIOR APPLICATION NUMBER: US/09/170,496
PRIOR PLING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                               172 BAW---DPASAGPARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGG 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                226 LEFRKDQLAILLPVRLEMAVVLFVVPLIITSYCYSRLVWILGRGG-SHRRQRRVAGLLAA 284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52 DILLITVSLPLKAVEALASGAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFP 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112 LGYQAFRRPCYSWGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCL 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MDLPPQLS------FGLYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCS
                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             229 ALLTLLLCVGPYNASNVASFLYPNLGGSWRKLGLITGAWSVVLNPLVTGYLGRG
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                                                                                                                                                        21.9%; Score 347; DB 14; Length 4 32.3%; Pred. No. 7.9e-24; ive 41; Mismatches 134; Indels
                   OTHER INFORMATION: MAP TO U62631.1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.4
OTHER INFORMATION: SWISSPROT HIT: 014843, EVALUE 0.00e+00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 32.04
Matches 94; Conservative
                                                                                                                                                                                  Best Local Similarity 32.33
Matches 95, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-251-385-274
                                                                            ; OTHER INFORMATIC
US-10-029-386-33898
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                                                                                                                                                           Query Match
FEATURE:
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Search completed: April 29, 2004, 12:17:26 Job time : 48 secs
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SOFTWARE: Patentin version 3.1
SEQ ID NO 467
LENGTH: 330
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nes 93; Conservative
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; ORGANISM: Homo sapiens
US-10-225-567A-467
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Best Local S:
Matches 93,
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Publication No. US20030105292A1
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Law, Chen W.
TITLE OF INVENTION: Receptors
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/10/251,385
CURRENT FILING DATE: 1998-10-13
               APPLICANT: Dong, Qu
TITLE OF INVENTION: Action Associated Factors as Targets for Treating
TITLE OF INVENTION: Atopic Allergies Including Asthma and Related Disorders
FILE REFERENCE: 036970-5072
CURRENT TILING DATE: 2003-01-22
CURRENT APPLICATION NUMBER: US/10/348,190
FRIOR APPLICATION NUMBER: US/09/157,24
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: EARLIER APPLICATION NUMBER: 60/059,510
PRIOR FILING DATE: EARLIER APPLICATION NUMBER: 60/032,224
PRIOR FILING DATE: EARLIER FILING DATE: 1996-12-02
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132 VAWVMSFGHCTIVIIVQ-----YLNTTEQVR---SGNEITCYENFTDNQLDVVLPVRL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLSLLLPFLPLAITAFCY---VGCLRALARSGLTHRRKLRAAWVAGGALLTLLLCVGPYN 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 ELCLVLFFIPMAVTIFCYMRFVWIMLSQPHVGAQRRR--RAVGLAVVTLLNFLVCFGPYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 YVAAFALGFPLNVLAIRGATAHARL-RLTPSLVYALNLGCSDLLLTVSLPLKAVEALASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71 AWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRPCYSWGVCAAI
                                                                                                                                                                                                                                                                                                                                                                                   21.1%; Score 334; DB 14; Length 330;
31.0%; Pred. No. 1e-22;
tive 53; Mismatches 120; Indels 34; Gaps
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Nicolaides, Nicholas
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SEQ ID NO 258
LENGTH: 330
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Best Local Similarity 31.0
Matches 93, Conservative
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; ORGANISM: Homo sapiens
US-10-251-385-258
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; ORGANISM: Homo sapiens
US-10-348-190-4
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Best Local Similarity
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US-10-251-385-258
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APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Bromer, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS FILE REFERENCE: 1920-4-4
                                                                                                                                                                                                                                                                                                                                                          241
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   12 YVAAFALGFPLNVLAIRGATAHARL-RLTFSLVYALNLGCSDLLLTVSLPLKAVEALASG
                              182 ELCLVLFFIPWAVTIFCYWRFVWIMLSQPLVGAQRRR--RAVGLAVVTLLNFLVCFGPYN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/225,567A CURRENT FILING DATE: 2001-12-19 PRIOR APPLICATION NUMBER: 60/257,144 PRIOR FILING DATE: 2000-12-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 467, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
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GenCore version 5.1.6
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 protein search, using sw model OM protein Run on:

April 29, 2004, 12:08:54 ; Search time 23 Seconds (without alignments) 673.382 Million cell updates/sec

US-10-202-687-2 1584 1 MDLPPQL&FGLYVAAFALGF......RGPGLKTVCAARTQGGKSQK 300

Title: Perfect score;

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

389414 seqs, 51625971 residues Searched:

389414 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued Patents AA:*

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(cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

(cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

(cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

(cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		de			SUMMAKIES	
Result No.	Score	Query. Match	Query. Match Length	03	αI	Description
П	1584	100.0	300	4	-09-170-4	Sequence 250, App
7	1579	99.7	300	4	US-09-170-496D-272	272,
m	347	21.9	346	4	US-09-170-496D-254	254,
4	347	21.9	401	~	US-08-820-521-2	2, Ar
5	347	21.9	401	m	US-09-248-715-2	7
9	347	21.9	401	m	US-09-248-715-2	Sequence 2, Appli
7	342	21.6	346	4	US-09-170-496D-274	274
œ	340.5	21.5	330	m	US-09-187-710-2	Sequence 2, Appli
σ	332	21.0	330	7	US-08-788-750-2	7
10	332	21.0	330	4	US-09-170-496D-258	258
11	331	20.9	330	4	US-09-170-496D-276	276
12	322	20.3	330	4	US-09-152-060-104	è
13	231.5	14.6	385	m	US-09-053-866-2	Sequence 2, Appli
14	231.5	14.6	385	4	US-09-479-130-2	7
15	231.5		385	4	US-09-472-130A-2	7
16	228	14.4	425	Н	US-07-657-769B-69	69
17	228	14.4	425	Н	US-08-097-938-7	۲,
18	228	14.4	425	Н	US-08-313-553-13	13
19	228	14.4	425	Н	US-07-789-184-220	Sequence 220, App
20	228	14.4	425	Н	US-08-476-000-7	7
21	228	14.4	425	Н	US-08-475-263-220	22
22	228	14.4	425	-	US-08-472-840-7	
23	228	14.4	425	-	US-08-485-886-220	22
24	228	14.4	425	~	US-08-477-362-220	220,
25	228	14.4	425	~	US-08-477-134-220	22
56	228	14.4	425	~	US-08-911-320A-3	Sequence 3, Appli
27	228	14.4	425	7	US-08-476-976-7	Sequence 7, Appli

RESULT 2 US-09-170-496D-272 'Sequence 272, Application US/09170496D 'Patent No. 6555339

7, Appli	57, Appl	13, Appl	220, App	7, Appli	220, App	3, Appli	220, App	7, Appli	186, App	40, Appl	2, Appli	2, Appli	3, Appli	6, Appli	56, Appl	380, App	56, Appl
Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence
US-08-742-440A-7	US-08-560-098A-57	US-08-767-993-13	US-08-473-489A-220	US-08-474-410-7	US-08-485-695-220	US-09-217-101-3	US-08-018-760-220	US-08-486-673B-7	US-09-170-496D-186	US-09-170-496D-40	US-09-041-545-2	US-09-327-925-2	PCT-US95-07180-3	US-08-742-440A-6	US-08-513-974B-56	US-08-513-974B-380	US-09-461-436B-56
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425	425	425	425	425	425	425	425	425	358	358	358	358	357	408	328	328	328
14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.2	13.7	13.4	13.4	13.3	13.0	12.8	12.8	12.8
228	228	228	228	228	228	228	228	228	225.5	216.5	213	213	210	205.5	202.5	202.5	202.5
28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Segura Donors 200 Application US/09170496D

Patent No. 655539
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Behan Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-CTILE REFERENCE: AREN-0040
CURRENT PAPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
SEQ ID NO 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 NASNVASFLYPNLGGSWRKLGLITGAWSVVLNPLVTGYLGRGPGLKTVCAARTQGGKSQK 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 PARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGGALLTLLLCVGPY
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100.0%; Pred. No. 3.2e-126;
ative 0; Mismatches 0;
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Best Local Similarity 100.
Matches 300; Conservative
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US-09-170-496D-250
RESULT 1
US-09-170-496D-250
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56 MDTGPDQSYFSGNHWFVFSVYLLTFLVGLPLNLLALVVFVGKLQRRPVAVDVLLLNLTAS 115
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                                                       112 LGYQAFRRPCYSWGVCAAIWALVLCHLGLVFGLBAPGGWLDHSNTSLGINTPVNGSPVCL 171
                                                                                                                                                              172 EAW---DPASAGPARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGG 228
                                                                                                                                                                                             61 DLLLLLFLPFRMVEAANGMHWPLPFILCPLSGFIFFTTIYLTALFLAAVSIERFLSVAHP 120
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                                                                                                                                                                                                                                                                                                    230 TLLNFLVCFGPYNVSHVVGYICGE-SPAWRIYVTLLSTLNSCVDPFVYYFSSSG 282
                                                                                                                                                                                                                                                                      229 ALLTLLLCVGPYNASNVASFLYPNLGGSWRKLGLITGAWSVVLNPLVTGYLGRG
                                                                                                    121 LWYKTRPRLGQAGLVSVACWLLASAHCSVVYVIÈFSGD-ISHSQGTNG----
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APPLICANT: Bergama, Derk
APPLICANT: Ganesh, Sathe
APPLICANT: Ganesh, Sathe
APPLICANT: Mao, Joyce
APPLICANT: Moo, Joyce
TITLE OF INVENTION: CDNA CLONE HNEDY20 THAT ENCODES
TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCES: 2
ADDRESSES: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 401;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: 1BM Compatible
OPERATING SYSTEM: DOS
SUFTWARE: FastsEQ for Windows Version 2.0
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/820,521
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08820521
Patent No. 5942416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Han, William T
REGISTRATION NUMBER: 34,344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: G
TELECOMMUNICATION INFORMATION
TELEPHONE: 610-270-5219
TELEPAX: 610-270-4026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 19-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acid
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-820-521-2
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US-09-170-496D-254
INFORMATION:
Sequence 254, Application US/09170496D
Sequence 254, Application US/09170496D
Sequence 255339
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
ITILE OF INVENTION: No. 655339-Endogenous, Constitutively Activated Human G Protein-III REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
SOFTWARE: Patentin version 3.1
SEQ. ID NOS: 294
SEQ. ID NOS: 294
SEQ. ID NOS: 294
SEQ. ID NOS: 294
                   APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN 0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
SEQ ID NO 272
LENGTH: 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 CYSWGVCAAIWALVLCHIGLUFGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAWDPASAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 LKAVEALASGAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRP 120
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32.3%; Pred. No. 1.1e-21;
tive 41; Mismatches 134; Indels 24; Gaps
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Pred. No. 8.5e-126;
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Best Local Similarity 99.7%;
Matches 299; Conservative (
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Best Local Similarity 32...
Best Local Similarity
Local Similarity
Local Similarity
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US-09-170-496D-272
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US-09-170-496D-254
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                                                                                                                                 225
                                                                                                                                                                                                    172 EAW----DPASAGPARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGG 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    115
116 DLLLLLFLPFRMVEAANGMHWPLPFILCPLSGFIFFTTIYLTALFLAAVSIERFLSVAHP 175
                                                                  112 LGYQAFRRPCYSWGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCL 171
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                                                                                                            56 MDTGPDQSYFSGNHWFVFSVYLLTFLVGLPLNLLALVVFVGKLQRRPVAVDVLLLNLTAS
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                                                                                                                                                                                                                                                                                                                                      229 ALLTILLCVGPYNASNVASFLYPNLGGSWRKLGLITGAWSVVLNPLVTGYLGRG 282
                                                                                                                                                                                                                                                                                                                                                                                285 TLLNFLVCFGPYNVSHVVGYICGE-SPAWRIYVTLLSTLNSCVDPFVYYFSSSG 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAO, JOYCE
TITLE OF INVENTION: CDNA CLONE HNFDY20 THAT ENCODES
ON TOWNSHINGENERS RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 401;
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FactSEQ for windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/248,715
FILING DATE: 09-Feb-1999
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/820,521
FILING DATE: 19-MAR-1997
ATTORNEY: ACENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GP-50011-1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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32.3%; Pred. No. 1.4e-21;
tive 41; Mismatches 134
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TOPOLOGY: linear
SEQUENCE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-248-715-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09248715
Patent No. 6277960
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SATHE, GANESH M.
FUETTERER, WENDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 610-407-0700
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 32.3
Matches 95; Conservative
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US-09-248-715-2
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116 DLLLLLFLPFRMVEAANGMHWPLPFILCPLSGFIFFTTIYLTALFLAAVSIERFLSVAHP 175
                                                                                                            172 EAW---DPASAGPARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGG 228
                                                                                                                                                                                                                                          226 LEPRKDQLAILLPVRLEMAVVLFVVPLIITSYCYSRLVWILGRGG-SHRRQRRVAGLLAA 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DLLLTVSLPLKAVEALASGAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFP 111
                                                                  LGYQAFRRPCYSWGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCL 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MDLPPQLS-----FGLYVAAFALGPPLNVLAIRGATAHARLRLTPSLVYALNLGCS
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                                                                                                                                                                                                                                                                                                                                      229 ALLTILLCVGPYNASNVASFLYPNLGGSWRKLGLITGAWSVVLNPLVTGYLGRG 282
                                                                                                                                                                                                                                                                                                                                                                            285 TLLNFLVCFGPYNVSHVVGYICGE-SPAWRIYVTLLSTLNSCVDPFVYYFSSSG 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09248715
Patent No. 6207800
| GENERAL INFORMATION:
APPLICANT: BERGSMA, DERK
APPLICANT: SATHE, GANESH M.
APPLICANT: FUETTERER, WENDY
| APPLICANT: PUETTERER, WENDY
| TITLE OF INVENTION: CDNA CLONE HNFDY20 THAT ENCODES
| TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR
| NUMBER OF SEQUENCES: 2
| CORRESPONDENCE ADDRESS: ADDRESSE: Ratner & Prestia
| STREET: P.O. Box 980
| CITY: Valley Forge
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APPLICATION NUMBER: US/09/248,715
FILING DATE: 09-FEB-1999
CLASSIFICATION:
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APPLICATION NUMBER: 08/820,521
FILING DATE: 19-MAR-1997
ATTONNEY AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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Best Local Similarity
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US-09-248-715-2
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71 AWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRPCYSWGVCAAI 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 --WALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAWDPASAG---PARFS 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSLLLFFLPLAITAFCY---VGCLRALARSGLTHRRKLRAAWVAGGALLTLLLCVGPYNA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 LCLVLFFVPMAVTIFCYWRFVWIMLTQPHVGAQRRR--RAVGLAVVTLLNFLVCFGPYNM 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                           12 YVAAFALGFPLNVLAIRGATAHARL-RLTPSLVYALNLGCSDLLLTVSLPLKAVEALASG
                                                                                                                                                                                                                                                                                                                                                                              47; Gaps
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Patent No. 5910430
GENERAL INFORMATION:
APPLICANT: Ellis, Catherine
APPLICANT: Bergsma, Derk
TITLE OF INVENTION: No. 5910430el G-Protein Coupled Receptor
TITLE OF INVENTION: (HTADX50)
                                                                                                                                                                                                                                                                                                                     Length 330;
                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                  DB 3;
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                                                                                                                                                                                                                                                                                                                  Score 340.5; DB Pred. No. 3.8e-21
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: DBM COMPATIBLE
COMPUTER: DOS
SOFTWARE: FASTERQ FOR WINDOWS VERSION 2.0
CURRENT APPLICATION DATA:
FILLING DATE: 24-JAN-1997
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CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CURRENT APPLICATION NUMBER: US/09/187,710A
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
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REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: ATGS0048
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ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 30.9
Matches 99; Conservative
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APPLICATION NUMBER:
                                                                                                                                                                                                                  , ORGANISM: HOMO SAPIENS
US-09-187-710-2
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                                                                                                                                                            LENGTH: 330
TYPE: PRT
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STATE:
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APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
FITLE OF INVENTION: Receptors
172 EAW----DPASAGPARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGG 228
                                                                                                                                                                                                                                                        DILLITVSIPIKAVEALASGAWPIPASICPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFP 111
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                                                                                            LGYQAFRRPCYSWGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCL 171
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| Sequence 2, Application US/09187710A
| Patent No. 6180365
| General No. 6180365
| APPLICANT: LANE, PAMELA
| APPLICANT: ELSHOURBAGY, NABIL
| APPLICANT: ELSHOURBAGY, NABIL
| APPLICANT: WHYER, LISA
| TITLE OF INVENTION: MOUSE 7-TRANSMEMBRANE RECEPTOR GPR43
| FILE REFERENCE: GP-70566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41; Mismatches 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/170,496D CURRENT FILING DATE: 1998-10-13 NUMBER OF SEQ ID NOS: 294 SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 274, Application US/09170496D
Patent No. 6555339
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US-09-170-496D-274
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Best Local Similarity
Matches 94; Conserv
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LENGTH: 346
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APPLICANT: Behan, Dominic P.
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Law, Chen W.
TITLE OF INVENTION: No. 655339-Endogenous, Constitutively Activated Human G Protein-C
TITLE OF INVENTION: Receptors
FILE REFERENCE: ARRN-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: PatentIn version 3.1
SEQ ID NO 276
LENGTH: 330
                                     240 VSHLVGY-HQRKSPWWRSIAVVFSSLNASLDPLLFYFSSSVVRRAFGRGLQVL---RNQG 295
     185 SLSLLLFFLPLAITAFCY---VGCLRALARSGLTHRRKLRAAWVAGGALLTLLLCVGPYN 241
                                                                                                                    242 ASNVASFLYPNLGGSWRKLGLITGAWSVVLNPLVTGYLGR-----GPGLKTVCAARTQG 295
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FILE REFERENCE: PZ003P1.US
CURRENT APPLICATION NUMBER: US/09/152,060
CURRENT FILING DATE: 1998-09-11
EARLIER PILING DATE: 1998-03-12
EARLIER PILING DATE: 1998-03-14
EARLIER PILING DATE: 1997-03-14
EARLIER APPLICATION NUMBER: 60/040,710
EARLIER APPLICATION NUMBER: 60/050,934
EARLIER APPLICATION NUMBER: 60/050,934
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                                                                                                                                                                                                                                                                                                           Sequence 276, Application US/09170496D Patent No. 6555339 GENERAL INFORMATION:
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Best Local Similarity 31.0
Matches 93; Conservative
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US-09-170-496D-276
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Patent No. 6555339
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Behan Dominic P.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-TITLE OF INVENTION: WHORER IS 1990-10-13
FILE REFERENCE: AREN-0040
CURRENT PILING DATE: 1999-10-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 ELCLVLPFIFWAVTIFCYWRFVWIMLSQPLVGAQRRR--RAVGLAVTLLNFLVCFGPYN 239
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;; Pred. No. 2e-20;
53; Mismatches 120; Indels 34;
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                                                                                                                                                                                                                                                                                                              21.0%;
31.0%;
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                                                                                       ä
TELEPHONE: 610-270-5219
TELEFAX: 610-270-4026
                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 330 amino acids
TYPE: amino acid
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Best Local Similarity 31...
Best Local Similarity 31...
And 93, Conservative
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TOPOLOGY: linear
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CORGANISM: Homo sapiens
US-09-170-496D-258
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Best Local Similarity
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US-09-170-496D-258
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                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
MAMB/KEY: SITE
LOCATION: (147)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: SITE
LOCATION: (181)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: (260)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-152-060-104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 AWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRPCYSWGYCAAI 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185 SLSLLLFFLPLAITAFCY---VGCLRALARSGLTHRRKLRAAWVAGGALLTLLLCVGPYN 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 ASNVASFLYPNLGGSWRKLGLITGAWSVVLNPLVTGYLGR-----GPGLKTVCAARTQG 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131 --WALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPV-CLEAWDPASAG---PARF 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 YVAAFALGFPLNVLAIRGATAHARL-RLTPSLVYALNLGCSDLLLTVSLPLKAVEALASG 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: SITE
LOCATION: (190)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 20.3%; Score 322; DB 4; Length 330; Best Local Similarity 31.0%; Pred. No. 1.4e-19; Matches 93; Conservative 50; Mismatches 123; Indels
EARLIER FILING DATE: 1997-05-30
FEARLIER PILING DATE: 1997-05-30
EARLIER APPLICATION NUMBER: 60/048,357
EARLIER APPLICATION NUMBER: 60/048,189
EARLIER FILING DATE: 1997-05-30
EARLIER PILING DATE: 1997-05-30
EARLIER PILING DATE: 1997-05-05
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER APPLICATION NUMBER: 60/068,368
EARLIER APPLICATION NUMBER: 60/068,368
EARLIER FILING DATE: 1997-12-19
SCATWARE: FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 118
SCOTUMARE: PARENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION:
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----VLCHLGLVFGLEAPGGWLDHSNTSLG 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---SHWQPAFT-----CLALLGCFLPLLAMILCYGATLHTLAASGRRYGHA 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 KAVEALASGAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRPC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 RIAYHLRGQRWPFGEAACRLATAALYGHMYGSVLLLAAVSLDRYLALVHPLRARALRGRR 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 LPPOLSFGLYVAAFALGFPLNVLAIRG-ATAHARLRLTPSLVYALNLGCSDLLLTVSLPL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                192 LALGLCMAAWLMAAALALPLTLQRQTFRLARSDRVLCHDALPLDAQA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----AAWVAGGALLTLLLCVGPYNAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 113; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----DKVRAGLFQRSPGDTVASKASAEGG 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 NVASFLYPNLGGSWRKLGLITGAWSVVLNPLVTGYLGRGPGLKTVCAARTQGG 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
14.6%; Score 231.5; DB 3; Length 385;
Best Local Similarity 24.9%; Pred. No. 7.3e-12;
Matches 88; Conservative 29; Mismatches 123; Indels 113
         PROTEASE-ACTIVATED RECEPTOR
PAR4 (2CHEMR2)
12
                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/053,866
FILING DATE:
                                                                                                                 ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Leith, Debra R
REGISTRATION NUMBER: 32,619
REFERENCE/DOCKET NUMBER: 98-1
TELECHONE: 206-442-6674
TELEPHONE: 206-442-6674
                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 385 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 YSWGVCAAIWAL----
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APPLICANT: Foster, Dona-
TITLE OF INVENTION: PRO-
TITLE OF INVENTION: PAR-
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239 -----
                                                                                                                                                                CITY: Seattle
STATE: WA
                                                                                                                                                                                                                 USA
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RESULT 14 US-09-479-130-2 ; Sequence 2, Application US/09479130

Sequence 2, Application US/09053866
Patent No. 6111075
GENERAL INPORMATION:
APPLICANT: Xu, Wenfeng
APPLICANT: Presnell, Scott R.
APPLICANT: Yee, David P.

US-09-053-866-2

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APPLICANT: Xu, Wenfeng
APPLICANT: Presnell, Scott R.
APPLICANT: Pee, David P.
APPLICANT: Yee, Donald C.
APPLICANT: FOSTER, Donald C.
ITILE OF INVENTION: PROTEASE-ACTIVATED RECEPTOR PAR4
ITILE OF INVENTION: (ZCHEMR2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REPERENCE: 98-10D2
CURRENT APPLICATION NUMBER: US/09/472,130A
CURRENT FILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: US 99/053,866
PRIOR PILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PastSEQ for Windows Version 3.0
SSOFTWARE: PastSEQ for Windows Version 3.0
ENGTH: 385
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                                                                                                                                            Sequence 2, Application US/09472130A Patent No. 6473765 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 YSWGVCAAIWAL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                 JS-09-472-130A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                239 -----SHWQPAFT----CLALLGCFLPLLAMLLCYGATLHTLAASGRRYGHA 281
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|------337
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14.6%; Score 231.5; DB 4; Length 385;
Best Local Similarity 24.9%; Pred. No. 7.3e-12;
Matches 88; Conservative 29; Mismatches 123; Indels 113;
Patent No. 6436400
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ye, Wenfeng
APPLICANT: Ye, David N
APPLICANT: Ye, David C
TITLE OF INVENTION: PROTEASE-ACTIVATED RECEPTOR
TITLE OF INVENTION: PRAR4 (2CHEMR2)
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: WA
COUNTRY: USA
ZIP: 98102
ZOPERTIER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Past:SEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Bastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/479,130
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98-10
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 YSWGVCAAIWAL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Leith, Debra K
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 385 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 206-442-6678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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0900Y4 08N6T6 035797 095ZA4 095XA0 090ZZQ 0712S9 08AXM7 090ZZO 090ZZO 091ZZO 090ZZO 09	ALIGN	Grat Sci	GPR40 Ligan he EMBL/Gen he EMBL/Gen 1; l to membra in-like rec in coupled _Rhodpsn. OPSN. OPSN.	Score 1329; Pred. No. 4 17; Mismatch
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1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	T 1 5 QBK3T5	OBASTS; OBASTS; O1-OCT-2002 (TrEMBL: O1-OCT-2003 (TrEMBL: GPR-0. GPR-0. GPR-0. Mus musculus (Mouse Eukaryota; Metazoa; Mammalia; Eutheria; MCBI_TaxID=10090; (1) SEQUENCE FROM N.A. STRAIN-BALB/C;	Andrews J.L., Briscoe C.P., Ignar D.M., M. Tadadyyon M.; Tadadyyon M.; Tadadyyon M.; Submitted of Screening for GPR40 Ligands."; Submitted (SFP-2002) to the EMBL/GenBank/I SEQUENCE FROM N.A. STRAIN=BALB/C; Blis C., Bishourbay N.; Submitted (AUG-2002) to the EMBL/GenBank/I EMBL; AFS39809; AAN03478.1; GO; GO:0010584; F:rhoddpsin-like receptor GO; GO:0001884; F:rhoddpsin-like receptor GO; GO:0001886; P:G-protein coupled recept InterPro; IPR000276; GPCR_Rhodpsn. PRINTS; PR00037; GFCRRHODOPSN. PROSITE; PS50262; G_PROTEIN RECEP F1_2; 1. SEQUENCE 300 AA; 31837 NW; AFF180P1688	Query Match Best Local Simi Matches 248;
11112222222222222222222222222222222222	SG.	54444888888888888888888888888888888888	445	Que: Best Matc

MDLPPQLSFGLYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCSDLLLTVSLP

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SEQUENCE FROM N.A.
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10 01-M

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Ellis C.E., Elshourbagy N.;
Ellis C.E., Elshourbagy N.;
Ellis C.E., Elshourbagy N.;
Submitted CAG-2003, to the EMBL/GenBank/DDBJ databases.
EMBL; AF539810; AAN03479.1; -.
EMBL; AF539810; AAN03479.1; -.
EG; GO:0010584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
InterPro; IPR000276; GPCR_Rhodpsn.
Fram; PR00037; GPCR_Rhodpsn.
PRINTS; PR00237; GPCR_Rhodpsn.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
SEQUENCE 300 AA; 31835 MW; 4E882AB259A5DD4F CRC64;
LKAVEALASGAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                181 PARLSPSILLFFLPLVITAFCYVGCLRALVRSGLSHKRKLRAAWVAGGALLTLLLCLGPY
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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81.7%; Pred. No. 2.2e-98;
ive 19; Mismatches 36; Indels 0
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Last sequence update)
Last annotation update)
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Matches 245; Conservative
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SEQUENCE FROM N.A.
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GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:001847; F:receptor activity; IEA.

GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

GO; GO:0001286; P:rhodopsin-like receptor protein signalin. . .; IEA.

InterPro; IPR000276; GPCR.Rhodopsn.

Pfam; PF0001; Tem 1; 1.

PROSITE; PS00237; GPCRHODOPN.

PROSITE; PS00237; GPRHODOPN.

PROSITE; PS00237; GPRPHODOPN.
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STRAINECTRE, 6J; TISSUE=COlon;
STRAINECTRE, 6J; TISSUE=COlon;
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The RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
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                                    QBVCK6, (TEMBLrel. 20, Created) (1-MAR-2002 (TEMBLrel. 20, Last sequence update) (1-MAR-2002 (TEMBLrel. 20, Last sequence update) (1-JUN-2003 (TEMBLrel. 24, Last annotation update) Similar to G protein-coupled receptor 43 (Orphan GPCR protein). GPR43 OR LSSIG. Muse). Bukaryota, Mctazoa; Ghordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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"LSGIG is a novel murine leukocyte specific GPCR that is induced the activation of STAT3.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases
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330 AA
PRT;
PRELIMINARY;
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XR MEDLINE=22354683; PubMed=12466851;
XR The FANTOM Consortium,
A The FANTOM Consortium,
A the RIKEN Genome Exploration Research Group Phase I & II Team;
A the RIKEN Genome Exploration Research Group Phase I & II Team;
A the RIKEN Genome Exploration Research Group Phase I & II Team;
A thanlysis of the mouse transcriptome based on functional annotation of RT "Analysis of the mouse transcriptome based on functional annotation of RT "Analysis of the mouse transcriptome based on functional annotation of RT "Analysis of the mouse transcriptome based on functional annotation of RT "Analysis of the mouse transcriptome based on functional annotation of RT "Analysis PSC154.57.12.00.

EMBL; AKO151298207; F2713.

DR GO; GO:0001584; F:Thodopsin-like receptor activity; IEA.

GO: GO:0001584; F:Thodopsin-like receptor activity; IEA.

GO; GO:0001186; P:G-protein coupled receptor protein signalin. . .; IEA.

InterPro; IPR000276; GPCR_Rhodpsn.

DR PROSITE; PSC00237; GPROTEIN RECEP_F1_1; 1.

DR PROSITE; PSC00237; GPROTEIN RECEP_F1_1; 1.

DR PROSITE; PSC00237; GPROTEIN RECEP_F1_2; 1.

SEQUENCE 396 AA; 42785 MW; DCIOSOE287AAE1B86 CRC64;
 ----TGYL 279
                          241 SHLVGF-YLRQSPSWRVEAVVFSSLNASLDPLLFYFSSSVVRRAFGKGLLLIRNPASSML 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 KAVEALASGAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRPC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 YSWGVCAAIW-----ALVLCHLGLVPGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAWD 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 204 LTTGLCLVAWLSAATLALPLTLHRQTFRLAGSDRMLCHDALPLTEQT-----SHWR 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 PASAGPARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGGALLTLLL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        255 PAF----ICLAVLGCFVPLLAMGLCYGATLRALAANGQRYSHALRL-----TALVLFS 303
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.0%; Score 222.5; DB 11; Length 396; 31.1%; Pred. No. 5.9e-10; ive 27; Mismatches 131; Indels 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 304 AVASFTPSNVLLVLHYSNPSPEAW---GNLYGAYVPSLALSTL 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      236 CVGPYNASNVASFL-YPNLG-GSWRKLGLITGAW--SVVLNPL 274
                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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243 SNVASFLYPNLGGSWRKLGLITGAWSVVLNPLV-
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                                                                                                                                                                                        Created)
                                                                                  300 GRG-AKETVEGTKMDRGGSQ 318
                                                        GRGPGLKTVCAARTQGGKSQ 299
                                                                                                                                                                                     01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                Protease-activated receptor
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hes 88; Conservative
                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hateh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Broaks S.A., McZwan P.J., McKernan K.J., Malke J.A., Gunarane P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
T. "Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148 WLLLLTALSPLARTD-----LTYPVHALGIIT-----CFDVLKWTMLPSVAMWAVFLF 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29 VYSLVAAVSIPGNLFSLWYLCRRMGPR-SPSVIFWINLSVTDLMLASVLPFQIYYHCNRH
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                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0001684; F:thodopsin-like receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PP00001; 7tm 1, 1, 1.
PRINTS; PR00237; GPCRRHODOPSN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 14.0%; Score 221.5; DB 4; Length Local Similarity 27.4%; Pred. No. 6.4e-10; nes 78; Conservative 47; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40635 MW; 565C43660B3C0CF7 CRC64;
        24, Last sequence update) 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22388257; PubMed=12477932;
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01-JUN-2003 (TrEMBLrel. 01-OCT-2003 (TrEMBLrel. Hypothetical protein. Homo sapiens (Human).
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359 AA; 4
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system of rainbow trout (Oncorhynchus
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 RPCYSWGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAW---- 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134 SPRKIFGICCTIWVLV------WIG-----SIPIYSFHGKVEKYMCFH 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                171 NMSDDTWSAKVFFPLEVFGFLLPMGIMGFC---CSRSI--HILLGRRDHTQDWVQQKA-- 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---DPASAGPARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGGALL 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DLPPQLSFGLYVAAFALGFPLNVLAIRGATAHARLR---LTPSLVYALNLGCSDLLLTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps

    [1] -
    SEQUENCE FROM N.A.
    Riryu I., Koellner B., Kuroda A., Ototake M., Dijkstra J.M.;
    "A new probable G-protein coupled receptor gene associated with the

                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G procein-coupled receptor rhodopsinL-1.
Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Bukaryote, Metazoa; Chordata; Cranatata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genew; HGNC.4511; GPR55.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0007186; F:receptor activity; IEA.

GO; GO:0007186; P:G-protein coupled receptor protein signalin.

InterPro; IPR000276; GPCR_Rhodpsn.

FFam; PF00001; 7tm 1; 1.

PRINTS; PR00237; GFCRH9DDSN.

PROSITE; PS00237; GFCRH9DDSN.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUB-Pancreas;
Straubberg R.;
Submitted (UN1-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC032694; AAH32694.1; -.
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                                                                                                                                                          Last sequence update)
Last annotation update)
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 209; DB 4;
Pred. No. 5.8e-09;
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                                                                319 AA
                                                                                                                                                                                                                       Similar to G protein-coupled receptor 55. Homo sapiens (Human).
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                                                                                                                             Created)
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Local Similarity 27.4%;
les 73; Conservative 3.
                                                                                                                      (TrEMBLrel. 22, (TrEMBLrel. 22, (TrEMBLrel. 25,
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                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                             01-OCT-2002
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SECUENCE
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                                                                                             Q8N580;
                                                                Q8N580
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             219 IGTLGTEEKHRIRGLILL--LMVIFILVLGPYHITGCVKYIGLLLHGDACEWEKTVFVPY 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94 GGFLAALSAGRYLGAAFPLGYQAFRRPCYSWGVCAAIWALVLCHLGLVFGLEAPGGWLDH 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38 LIPS----LVYALINIGCSDILLITVSLPLKAVEALASGAWPLPASLCPVFAVAHFFPLYAG 93
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases,
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases,
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001188; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001188; F:rhodopsin-like receptor protein signalin. .; IEA.
InterPro; IPR000276; GPCR_Rhodpsn.
Pram: PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODPSN.
PROSITE; PS00237; GPCRFIN_RECEP_F1_1; 1.
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001586; P:G-protein coupled receptor protein signalin. . .; IEA.
InterPro; IPR000276; GPCR_Rhodosn.
Pfam; PF00001; 7tm_1; 1.
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"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL; AK085829; BAC39547.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 SNTSLGINTPVNGSPVCLEAWDPASAGPARFSLSL--LLFFLPLAITAFCYVGCLR---A
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99
                                                                                                                                                                                                                                                                                                                                                                                                                           DB 13; Length 343;
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                                                                                                                                                                                                                                                                                                                                                                 343 AA; 38830 MW; 761F06E57F76BB40 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 9e-09;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence
01-OCT-2003 (TrEMBLrel. 25, Last annotati
Probable G protein-coupled receptor GPR4.
                                                                                                                                                                                                                                                                                                                                                                                                                           13.1%; Score 207;
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MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             260 -LGLITGAMSVVLNPLVTGYL 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      23.7%;
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40269 MW; FA9CAB7AA8BBD764 CRC64;
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Submitted (MAY-2003) to the
EMBL; BC052868; AAH52868.1;
       367 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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Q7TMV7
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                                                                                                                                                                                                                                                                                                                                                                     76 VDYFLHHDNWIHGPGSCKLFGFIFYSNIYISIAFLCCISVDRYLAVAHPLRFARLRRVKT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136 AVAVSSVVWA------------TELG----ANSAPLFHDELFRDRYNHT 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170 -CLEAWDPASAGPARFSLSLLL--FFLPLAITAFCYVGCLRALARSGLTHRR-KLRAAWV 225
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                                                                                                                                                                                                                                                   PP---SLYIFVIGVGLPTNCLAL--WAAYRQVRQHNELGVYLMNLSIADLLYICTLPLW 75
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001884; F:receptor activity; IEA.
GO; GO:0001886; F:receptor activity; IEA.
GO; GO:000186; P:G-protein coupled receptor protein signalin. .; IEA.
InterPro; IRR000276; GPCR_Rhodpsn.
Pfam; PP00001; 7tm.1; 1.
PROSITE; PS00237; GPCRRHODPSN.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_1; 1.
                                                                                                                                                                                                                       4 PPQLSFGLYVAAFALGFPLNVLAIRGATAHARLRLTPSL-VYALNLGCSDLLLTVSLPLK
                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                     123 SWGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPV------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ovis aries (Sheep).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoldea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Debus N.; "Regulation of GH secretion in sheep: Role of somatostatin and its
                                                                                                                                                                         55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Debus N., Dutour A., Boudouresque F., Vuaroqueaux V., Oliver C.
                                                                                                                       Query Match
Best Local Similarity 27.5%; Pred. No. 1e-08;
Matches 75; Conservative 35; Mismatches 108; Indels 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Department of Intercellular communications in Endocrinology University of Aix-Marseilles II, Marseilles, France.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor subtype 5: osst5.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
PROSITE; 365 AA, 41104 WW, 20D9P6128BE0EA37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-00T-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      226 AGGALLTLLLCVGPYNASNVA-SFLYPNLGGSW 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     228 ALSLIAIVLVCFAPYHALLLSRSAVY--LGRPW 258
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Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RETAINE-57BL/6NCT; TISSUE-Hematopoietic Stem Cell;
RETAINE-57380257; PubMed=12477932;
RA Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RIdusner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Ropkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenco L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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Richards S.W., McZwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Rahey J., Helton E., Ketreman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Richards A.C., Garimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Rodiguez A.C., Garimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Andriguez A.C., Garimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Andriguez A.C., Garimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Andriguez A.C., Garimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Andriguez A.C., Garimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Andriguez A.C., Garimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Andriguez A.C., Garimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Andriguez A.C., Garimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Andriguez A.C., Garimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Andriguez A.C., Garimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Andriguez A.C., Garimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Andriguez A.C., Garimwood J., Schmut J. J., Myers R.M., Butterfield Y.S.,
Andriguez A.C., Garimwood J., Schmut J. J., Myers R.M., Butterfield Y.S.,
Andriguez A.C., Garimwood J., Schmut J. J., Myers R.M., Butterfield Y.S.,
Andriguez A.C., Garim A.
                                                                                                                                                                                                                                                                     46 LYLLVCAVGLGGNALVIYVVLRHAKMK-TVTNIYILNLAVADVLLMLGLPFVATQN-AIS 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104 YWPFGPVLCRLVMTLDGINQFTSIFC----LTVMSVDRYLAVVHPIRSARWRRPRVAKLA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        203 IIYTSVLGFFGPLLVICLCYVLIVVKLKASGVRVGSTRRRSERK--VTRMVVVVVLVFAG 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               261 CWLPFFIVNIVNLAFALPEEPASAGLYFFVVVLSYANSCA-NPCLYGFLSDNLRQSFRKY 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 CAAIWAL-VLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAW-DPASAGPARF 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  160 SAAVWAFSLVWSLPLVVFADIQEGW-----NT-----CNLTWPEPVGLWGAVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185 SL--SLLLFFLPLAITAFCYVGCLRALARSGL----THRRKLRAAWVAGGALLTLLLCVG
                                                                                                                                                                                                           11 LYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCSDLLLTVSLPLKAVEALASG
                                                                                                                                                                                                                                                                                                                                                                                                                  71 AWPLPASICPVF----AVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRPCYSWGV
                                                                                                                  Gaps
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                  49;
               Length
                                                                                                                  Indels
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Last annotation update)
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STRAIN=C57BL/6NCr; IISSUE=Hematopoietic Stem Cell;
                                                                                                                  48; Mismatches 131;
          DB 6;
     12.8%; Score 203.5; DB 6 26.9%; Pred. No. 1.8e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                357 AA
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Query Match
Best Local Similarity 26.94
Matches 84; Conservative
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NCBI_TaxID=9606;
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SEQUENCE
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QBN5S7
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Matches
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                                                                                                                                                  153 ILVPAQTLPLP-------LTPMSKEEGDKTTCMEY--PNFEGTASLPWI 192
                                                                                                                                                                                                                                                    193 LLGACLLGYVLPITVILLCYSQICCKLFRTAKQNPLTEK----SGVNKKALNTIILIIV 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 LPLKAVBALASGAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFR 118
                                                                                                                                    72 WPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRPCYSWGVCAAIW 131
                                                                                                                                                                                     132 ALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVN----GSPVCLEAWDPASAGPAR---- 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78
                                                                                    71
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                                                                                                                                                                                                                                     184 -PSLSLLLPFLPLAITAFCY--VGC--LRALARSGLTHRRKLRAAWVAGGALLTL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 DLPPQLSFGLYVAAFALGFPLNVLAIRGATA---HARLRLTPSLVYALNLGCSDLLLTVS
                                                                                   12 YVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCSDLLLTVSLPLKAVEALASGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sawzdargo M., Nguyen T., Lee D.K., Lynch K.R., Cheng R., Heng H.H.Q., George S.R., O'Dowd B.F.;
"Identification and cloning of three novel human G protein-coupled receptor genes GPR52, PSI.GPR53 and GPR55: GPR55 is extensively Mol. Brain Res. 64:193-198(1999).
EMBL; AF100789; AAD22411.1;
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                            46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0016021; C:Integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001186; P:G-protein coupled receptor protein signalin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.6%; Score 199; DB 11; Length 29
25.8%; Pred. No. 3.4e-08;
ive 34; Mismatches 129; Indels
                                 ; Score 200; DB 11; Length 3:
; Pred. No. 3.4e-08;
38; Mismatches 103; Indels
Hypothetical protein.
SEQUENCE 357 AA; 40191 MW; 56B96775303FBDDF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34008 MW; 7D7A99596C21A030 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                      protein-coupled receptor (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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MEDLINE=99132385; PubMed=9931487;
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PRINTS; PR00237; GPCRRHODOPSN
                                    12.6%; 25.8%;
                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                    248 VFILCFTPYHVA 259
                                                                                                                                                                                                                                                                                      234 -- LLCVGPYNAS 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67; Conservative
                                                            65; Conservative
                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat)
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296 2
296 AA;
                                  Query Match
Best Local Similarity
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SEQUENCE
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79 LPFKMILPQVKSSPSL--VFCTFVECLYFISMYGSVFTICFISLDRLLAIQYPLLVNHFR 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     192 HALVSLA-VAPTFPPITTVTCYLLIRSL-RQGLRVEKRLKTKAVRMIAIVLAIFLVCFV 249
                                                                                              119 RPCYSWGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLGINT---PVNGSPVCLEAWD 175
                                                                                                                                                                                                                          176 PASAGPARFSLSLLLFFLPLAITAFC---YVGCLRALARSGLTHRRKLRAAWVAGGALLT 232
                                                                                                                                                                                                                                                                                 178 STWSARVPFPLEIFGFLLPMGIMGFCSYRSIHILLSIQGDDQWVRKRACIIWTIATNLVV 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 PARFSLSLLLFFLPLAITAFCYVGCLRALARSGL--THRRKURAAWVAGGALLTLLLCVG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, BC031653; AAH31653.1; -...

EMBL, BC031653; AAH31653.1; -...

GO, GO:0004872; F:receptor attivity, IEA.

GO, GO:000184; F:rhodopsin-like receptor activity; IEA.

GO, GO:000186; P:G-protein coupled receptor protein signalin. .; IEA.

InterPro; PR0027; GPCR.Rhodopsn.

Pfam; PR0021; 7Fm 1; 1.

PRINTS; PR00237; GPCRRHODOPSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33 LFASFYLLDF---ILALVGNT----LALWFFIRDHKSGTPANVFLMHLAVADLSCVLVLP
                                                                                                                                                         137 SPRKTFGICCIÍWMLV-------WG----SIPIYTFHRGVEGYKCFHNMSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 LYVAAFALGFPLNVLAIRGATAHARLRL------TPSLVYALNLGCSDLLLTVSLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.5%; Score 198; DB 4; Length 33: 26.6%; Pred. No. 4.7e-08; tive 41; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.; Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 339 AA; 37860 MW; BBOCAFDOFC371D63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
G protein-coupled receptor 17.
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                      233 LLLCVGPYNASNVASFLYPN 252
                                                                                                                                                                                                                                                                                                                                                                                                                238 FVVSFLPVHLGLFLQFLVRN 257
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TISSUE=Brain, and Lung;
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38; Gaps

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3 LPPQLSFGLYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNIGCSDLLLTVSLPLK
Heubner D., Mewes H.W., Weil B., Amid C., Osanger
                                                                                                                                     Length 376;
                                                                                                                                                                               42; Mismatches 145; Indels
                Fobo G., Han M., Wiemann S.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BK537386; CAD97628.1; -.
Hypothetical protein
SEQUENCE 376 AA; 42720 MW; 7638373C15A695DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.5%; Score 197.5; DB 11; 24.1%; Pred. No. 5.6e-08; ive 45; Mismatches 134;
                                                                                                                                     Query Match
12.5%; Score 198; DB 4;
Best Local Similarity 24.5%; Pred. No. 5.2e-08;
Matches 73; Conservative 42; Mismatches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        369 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proteinase activated receptor 3 precursor.
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The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 24.1
hes 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 AWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRPCYSWGVCAAI 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 WALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAWDPASAGPARFSLSLLL 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 AFP-----HULGYFLNMHCSILFLTCICVDRYLAIVQFEGSRRWRQPACAKAVCIFV 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 WLAA----GVV-----FALTVLE 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPLPLAITAFCYVGCLRALARSGLT---HRRKLRAAWVAGGALLTLLLCVGPYNASNVAS 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  204 PLLPLLVISVFTGRIMCALSRPGLLRQGRQRRVRAMQLLLTVLVIFLVCFTPFHARQVAV 263
                                                                                                                                                                                                                                                                                                                                                        60,770 full-length cDNAB.";

Nature 420:563-573 (2002).

EMBL; AR040547; BAC30623.1; -.

MGD; MGI:2441803; Gpr20.

GO; GO:001564; F:rhodopsin-like receptor activity; IEA.

GO; GO:0007186; F:G-protein coupled receptor protein signalin. .; IEA.

PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                     the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCSDLLLTVSLPLK-AVEALASG----
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                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 11; Length 358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.5%; Score 198; DB 11; Length 35: 28.0%; Pred. No. 5e-08; ive 41; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1_1; 1.
PROSITE; PS00262; G PROTEIN RECEP F1_2; 1.
SEQUENCE 358 AA; 39431 MW; C6F7042ABDE9CABF CRC64;
                                     U1-OCT-2003 (TrEMBLrel. 23, Last sequence update)
Putative G-protein coupled receptor homolog.

MNS musculne (Marchine)
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein DKFZp686N1782.
DKFZP686N1782.
358 AA
                                                                                                                                                                                                                                                        STRAIN=CS7BL/6J; TISSUB=Thymus;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
                                   01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 28.0%
les 69; Conservative
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PRELIMINARY;
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SEQUENCE FROM N.A.
TISSUE=Human retina;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              264 ALWPNV 269
                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                NCBI_TaxID=10090;
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150 IAYHLNGNNWVFGEVLCRATTVIFYGNWYCSILLLACISINRYLAIVHPFTYRGLPKHTY 209
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                                                                                                                                                                                                                                                                                                       123 SWGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLG--INTPVNGSPVCLEAWDPASAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        264 ---ISLAFFGFLIPFVLIIXCYAAIIRTL--NAYDH----RWLWYVKASLLILVIFTICF 314
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                                                                                                                                                                                                                                                                                                                                                                                           210 ALVICGLVWATVFLYMLPFFILKQBYYLVQPDITICHDVHNTCESSSPFQLYYF----- 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 PARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGGALLTLL---LCV 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 AVEALASGAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRPCY 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238 GPYNASNV---ASFLYPNLGGSW--RKLGLITGAWSVVLNPLV-----TGYL 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          315 APSNIILIIHHANYYYNNTDGLYFIYLIALCLGSLNSCLDPFLYFLMSKTRNHSTAYL 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The FAILOR Concerns Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,70 full-length cDNAs.";
Nature 420:563-573 (2002)
EMBL; AK089444; BAC40886.1; -.
MGD; MGI:1298208; FZI12.
MGD; MGI:1298208; FZI12.
MGO; MGI:1298208; FII C:integral to membrane; IEA.
MGO; MGI:1298208; F:integral to membrane; IEA.
MGO; MGI:12982082; GER_Rhodpsin-like receptor protein signalin. .; IEA
PEAN: PROMOUL; 7tm 1; 1.
PROSITE; PS50262; GEROTEIN RECEP FI 2; 1.
SEQUENCE 369 AA; 41696 MW; CBEGB009710519EF CRC64;
                                                                                                                         63 AVEALASGAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRPCY
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Search completed: April 29, 2004, 12:11:31 Job time : 47 $\ensuremath{\text{BecB}}$

us-10-202-687-2.rsp

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

April 29, 2004, 12:04:08; Search time 18 Seconds (without alignments) 867.836 Million cell updates/sec

Title: Perfect score: Sequence:

US-10-202-687-2 1584 1 MDLPPQLSFGLXVAAFALGF.....RGPGLKTVCAARTQGGKSQK 300

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% . Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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188.5	186.5 185.5 185.5	185 185 185 184.5	184.5 184 183.5
34 35	337	2 4 4 4 0 1 2	4 4 4 6 4 7

ALIGNMENTS

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                                                                                                                                                                                                                            61 LKAVEALASGAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRP 120
                                                                                                                                                                                                                                                                CYSWGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAWDPASAG 180
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                                                                                                                                                                                  9
                                                                                                                                                                         MDLPPQLSFGLYVAAFALGFPLAVTAIRGATAHARLRLTPSLVYALNLGCSDLLLTVSLP
                                                                                                                                                                                                                                                                                                                  PARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGGALLTLLLCVGPY
                                                                                                                                                                                                                                                                                                                                   181 PARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHRRKKLRAAWVAGGALLTLLLCVGPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Lamerdin J.E., McCready P.M., Adamson A.W., Burkhart-Schultz K.,
Garcia E., Kyle A., Ramirez M., Stilwagen S., Garnes J., Danganan L.,
Bruce R., Quan G., Montgomery M., Ow D., Kobayashi A., Olsen A.O.,
                                                                                                                                                          MDLPPQLSFGLYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCSDLLLTVSLP
                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Orphan receptor.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O'Dowd B.F.;
"A cluster of four novel human G protein-coupled receptor genes occurring in close proximity to CD22 gene on chromosome 19q13.1.";
Biochem. Biophys. Res. Commun. 239:543-547(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sawzdargo M., George S.R., Nguyen T., Xu S., Kolakowski L.F. Jr.,
                                      7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL)
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                                                                                                    ; Score 1584; DB 1; Length 300;
; Pred. No. 9.7e-111;
0; Mismatches 0; Indels 0
                                                                    TIEF27DACD93E80B CRC64;
             6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
 CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GP42 HUMAN STANDARD; PRT; 346 AA. 015529; 15-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Probable G protein-coupled receptor GPR42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=98008875; Pubmed=9344866;
                                                                             31457 MW;
                                                                                                      100.0%;
                                                                                                                  Best Local Similarity 100. Matches 300; Conservative
                                                  300
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198 2
222 2
243 2
259 2
280 3
155 1
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 DOMAIN
TRANSMEM
                                                  DOMAIN
CARBOHYD
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61 DILILIERPPRAVEAANGMEMPEPPILCPISGFIFFTIYITALFLAAVSIERFISVAHP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               171 LEAWDP--ASAGPARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGG 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                      MIM; 603822; -.
GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0004330; F:G-protein coupled receptor activity; TAS.
GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
InterPro; IPR000276; GPCR_Rhodpsn.
PF00001; 7tm_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 LWYKTRPRLGQAGLVSVACWLLASAHCSVVYVIEFSGD-ISHSQGTNG-----TCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          229 ALLTLLLCVGPYNASNVASFLYPNLGGS--WRKLGLITGAWSVVLNPLVTGYLGRG 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34.1%; Pred. No. 2.3e-20;
iive 38; Mismatches 129; Indels
                                                                                                                                                                                                                         PRINTS; PRO0237; GPCRRHODOPSN.
PROSITE; PS00237; GPROTEIN RECEP F1 1; 1.
PROSITE; PS002237; GPROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Transmembrane.
DOMAIN
TRANSMEM 20 40 1 (POTENTIAL).
TRANSMEM 41 47 CYTOPLASMIC.
TRANSMEM 48 68 2 (POTENTIAL).
DOMAIN 69 90 EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
5 (POTENTIAL).
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03F6742DA4B798D0 CRC64;
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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15-JUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
GPR41.
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MEDLINE=98008875; PubMed=9344866;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38695 MW;
EMBL, AF024689; AAB86712.1;
EMBL, AC002511; AAB67885.1;
PIR, JC5716; JC5716.
Genew, HGNC:4500; GPR42.
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346 AA;
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014843;
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SEQUENCE
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                                                                               . .; TAS.
                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
-1- FUNCTION: Orphan receptor.
-1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                  "A cluster of four novel human G protein-coupled receptor genes occurring in close proximity to CD22 gene on chromosome 19q13.1."; Biochem. Biophys. Res. Commun. 239:543-547(1997).
Sawzdargo M., George S.R., Nguyen T., Xu S., Kolakowski L.F. Jr.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MIM; 603821; -.
GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0004930; F:G-protein coupled receptor activity; TAS.
GO; GO:0007186; P:G-protein coupled receptor protein signalin.
InterPro; IPR00276; GPCR Rhodpsn.
PF00001; 7tm_1; 1.
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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Transmembrane.
1 19 EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC.
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38649 |
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346 AA;
                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00237;
                                                                            TISSUE=Ovary;
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CARBOHYD
SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                   112 LGYQAFRRPCYSWGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCL 171
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GO:0005887; C:integral to plasma membrane; TAS.
GO:0004810; F:G-protein coupled receptor activity; TAS.
GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
                                                                                                                                                                                DLLLTVSLPLKAVEALASGAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFP
                                                                                           1 MDLPPQLS------FGLYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCS
                                                                                                                                  1 MDTGPDQSYFSGNHWFVFSVYLLTFLVGLPLNLLALVVFVGKLQRRPVAVDVLLLNLTAS
                                                                                                                                                                                                                                                                                                                                                          172 EAW---DPASAGPARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Lamerdin J.B., McCready P.M., Adamson A.W., Burkhart-Schultz K.,
Lamerdin J.B., Kyle A., Ramirez M., Stilwagen S., Garnes J., Danganan L.,
Bruce R., Quan G., Montgomery M., Ow D., Kobayashi A., Olsen A.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         230 TLIANFLVCFGPYNVSHVVGYICGE-SPAMRIYVTLLSTLASCVDPFVYYFSSSG 282
                                                                                                                                                                                                                                                                                                                                                                                                                                               229 ALLTLLLCVGPYNASNVASFLYPNLGGSWRKLGLITGAWSVVLNPLVTGYLGRG 282
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-i- SUBCELLULAR LOCATION: Integral membrane protein.
-i- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    occurring in close proximity to CD22 gene on chromosome 19q13.1.";
Biochem. Biophys. Res. Commun. 239:543-547(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-98008875; PubMed-9344866;
Sawzdargo M., George S.R., Nguyen T., Xu S., Kolakowski L.F. Jr.
                                                24;
    21.9%; Score 347; DB 1; Length 346; 32.3%; Pred. No. 6e-19; ive 41; Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "A cluster of four novel human G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Probable G protein-coupled receptor GPR43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF024690; AAB86713.1; -.
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Query Match
Best Local Similarity 32.3
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     132 VAWVMSFGHCTIVIIVO-----YLNTTEQVR---SGNEITCYENFIDNQLDVVLPVRL 181
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01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Proteinase activated receptor 1 precursor (PAR-1) (Thrombin receptor).
Xenopus laevis (African clawed from the Company Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 YVAAFALGFPLNVLAIRGATAHARL-RLTPSLVYALNLGCSDLLLTVSLPLKAVEALASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 YIIFLTGLPANLLALRAFVGRIRQPQPAPVHILLSLTLADLLLLLLLLLLLLEASNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     242 ASNVASFLYPNLGGSWRKLGLITGAWSVVLNPLVTGYLGR-----GPGLKTVCAARTQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185 SLSLLFFLPLATTAFCY---VGCLRALARSGLTHRRKLRAAWVAGGALLTLLLCVGPYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21.0%; Score 332; DB 1; Length 330; 31.0%; Pred. No. 7.4e-18; ive 53; Mismatches 120; Indels
InterPro; 1Proco...

Pfam; PF00001; 7tm 1; 1.

PRINTS; PR00237; GPROTEIN RECEP F1 1; 1.

PROSITE; PS0262; GPROTEIN RECEP F1 2; 1.

G-procein coupled receptor; Transmembrane; Polymorphism.

1 2 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                    6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                              2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                   4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                              L -> H (in dbSNP:409093).
/FIId=VAR 011861.
                                                                                                                                                                                                                                                                                                                                                                                                                                                37143 MW; F4A8AC6AFBDF1E90 CRC64;
                                                                                                                                                                                                                                                                     5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 420 AA
                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 31.0%;
nes 93, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                              12
33
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62
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105
117
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1173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                330 AA;
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TRANSMEM
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
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     8
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 ---SLSLLLFFLPLAITAFCYVGCLRALARSGLTHR-RKLRAAWVAGGALLTLLLCVGFY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     269 YFSSFCLLFFFVPFIITTICYIGIIRSLSSSSIENSCKKTRALFLAVVVLCVFIICFGFT 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 AWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRPCYSWGVCAAI 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 WALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSP-----VCLEAWDPASAGPARP- 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 LYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCSDLLLTVSLPLKAVEALASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      226 WLISIA------STIPLLVTEQTQKIPRLDITTCHDVLDLKDFYIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166 DWLFGPGMCRIVTAIFYCNMYCSVLLIASISVDRFLAVVYPMHSLSWRTMSRAYMACSFI
coupled
                     G proteins that stimulate phosphoinositide hydrolysis.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- PTM: A proteolytic cleavage generates a new amino terminus that functions as a tethered ligand.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
K-A: LACK OF ACTIVATION BY THROMBIN.
D5163F56AFE12372 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0237; GPCRRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Signal; Blood coagulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       329 NVLFLTHYLQBANEFLYFAY-----ILSACVGSVSCCLDPLIYYY 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REMOVED FOR RECEPTOR ACTIVATION.
PROTEINASE ACTIVATED RECEPTOR 1.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 420;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 244; DB 1; Length 420; Pred. No. 3.1e-11; 44; Mismatches 126; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U09632; AAA18498.1; -.
BIR; ISIG67; ISIG67.
INTERPRO; IPRO00276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47435 MW;
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25.0%;
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Best Local Similarity 25.03
Matches 72; Conservative
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1101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   platelets by thrombin.";
J. Clin. Invest. 103:879-887(1999).
-!-FUNCTION: Receptor for activated thrombin or trypsin coupled to G proteins that stimulate phosphoinositide hydrolysis. May play a role in platelets activation.
-!- SUBCELLUIAR LOCATION: Integral membrane protein.
-!- TISSUE SPECTFICITY: Widely expressed, with highest levels in lung, pancreas, thyroid, testis and small intestine. Not expressed in brain, kidney, spinal cord and peripheral blood leukocytes. Also detected in platelets.
PAR4 HUMAN STANDARD; PRT; 385 AA.
Q96RIO, 076067;
28-PRB-2003 (Rel. 41, Created)
28-PRB-2003 (Rel. 41, Last sequence update)
28-PRB-2003 (Rel. 41, Last annotation update)
Proteinase activated receptor 4 precursor (PAR-4) (Thrombin receptor-like 3) (Coagulation factor II receptor-like 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTM: A proteolytic cleavage generates a new amino terminus that functions as a tethered ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUB=Lymphoma; William of 18465; William 1881. Yee D.P., Xu W.-F., Andersen H., Whitmore T.E., Presnell S.R., Yee D.P., Ching A., Gilbert T., Davie E.W., Foster D.C.; "Cloning and characterization of human protease-activated receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C.L., Yi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kahn M.L., Nakanishi-Matsui M., Shapiro M.J., Ishihara H.,
Coughlin S.R.,
"Protease-activated receptors 1 and 4 mediate activation of human
                                                                                                                                                                                Eukaryora, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŝ
                                                                                                                                                                                                                                                                                              MEDLINE=98389762; PubMed=9722561;
Kahn M.L., Hammes S.R., Botka C., Coughlin S.R.;
"Gene and locus structure and chromosomal localization of the
procease-activated receptor gene family.";
J. Biol. Chem. 273:23290-23296(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98379991; PubMed=9716134;
Kahn M.L., Zheng Y.-W., Huang W., Bigornia V., Zeng D., Moff
Farese R.V. Jr., Tam C., Coughlin S.R.;
"A dual thrombin receptor system for platelet activation.";
Nature 394:690-694(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND VARIANTS VAL-296 AND LEU-310. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel Nickerson D.A.; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND MUTAGENESIS OF ARG-47 AND ARG-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 95:6642-6646(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99178892; PubMed=10079109;
                                                                                                                                                                        Homo sapiens (Human).
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE PROM N.A.
                                                                                                                                                    2RL3 OR PAR4
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337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 RIAYHLRGQRWPFGEAACRLATAALYGHMYGSVLLLAAVSLDRYLALVHPLRARALRGRR 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----VLCHLGLVFGLEAPGGWLDHSNTSLG 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   160 INTPVNGSPVCLEAWDPASAGPARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHRRK 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----AAWVAGGALLTILLCVGPYNAS 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 LPPOLSFGLYVAAFALGFPLNVLAIRG-ATAHARLRLTPSLVYALNLGCSDLLLTVSLPL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    282 LRLTAVVLASAVAFFVPSNLLLLHYSDPSPSAWGNLYGAYVPSLALSTLNSCVDP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.6%; Score 231.5; DB 1; Length 385;
24.9%; Pred. No. 2.4e-10;
tive 29; Mismatches 123; Indels 113; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THROMBIN OR TRYPSIN).
R->A: NO BFFECT ON RECEPTOR ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192 LALGLCMAAWLMAAALALPLTLQRQTFRLARSDRVLCHDALPLDAQA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  244 NVASFLYPNLGGSWRKLGLITGAWSVVLNPLVTGYLGRGPGLKTVCAARTQGG 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----FIYYYVSAEFR-------DKVRAGLFQRSPGDTVASKASAEGG 373
                                                                               Interero; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRHODOPSN.
PROSITE; PS00237; GPROTEIN_RECEP_F1 1; 1.
PROSITE; PS50263; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLEAVAGE (BY THROMBIN OR TRYPSIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /FTId=VAR 012853.
R->A: NO PROTEOLYTIC CLEAVAGE (BY
                                                                                                                                                                                                                                                                                                               PROTEINASE ACTIVATED RECEPTOR 4.
                                                                                                                                                                                                                                                                REMOVED FOR RECEPTOR ACTIVATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                       2 (POTENTIAL).
EXTRACELLUIAR (POTENTIAL)
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41162 MW; FACA62B40D5756AE CRC64;
                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                           1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FTIG=VAR_012852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -> A (IN 'REF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY
                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                        Blood coagulation; Polymorphism. SIGNAL 17
EMBL; AF055917; AAC25699.1; -. EMBL; AF384819; AAK61908.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 YSWGVCAAIWAL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88; Conservative
                    EMBL; AF384819; AAK61908
Genew; HGNC:3540; F2RL3.
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385 AA;
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EMBL; AF080214; AAC28860.1; -.

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Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heibeh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A prapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Radriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Blakesley R.W., Krzywinski M.I., Skalska U., Smailus D.E.,

Rocherch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length

"Marna and mouse GDNA sequences.";

"Marna and mouse GDNA sequences.";

"Marna and mouse GDNA sequences.";

"Marna and mouse GDNA sequences.";
                                                                                                                                                                                                                                                                                                                       Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q., Nickerson D.A., Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Characterization of single-nucleotide polymorphisms in coding regions
                                    PARI HUMAN STANDARD; PRT; 425 AA.
P25116; OSERT; Q9BUN4;
01-MAY-1992 (Rel. 22, Created)
10-MAY-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
Protetainse activated receptor 1 precursor (PAR-1) (Thrombin receptor)
F2R OR PARI OR TR OR CF2R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N., Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L.,
                                                                                                                                                                                                              MEDLINE=91168254; PubMed=1672265; Vu T.-K.H., Hung D.T., Wheaton V.I., Coughlin S.R.; Vu T.-K.H., Hung D.T., Wheaton V.I., Coughlin S.R.; Molecular cloning of a functional thrombin receptor reveals a novel proteolytic mechanism of receptor activation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEDLINE=99318093; PubMed=10391209;
MEDLINE=99318093; PubMed=10391209;
Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L.
Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Protease-activated receptors 1 and 4 mediate activation of human platelets by thrombin."; J. Clin. Invest. 103:879-887(1999).
                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99178892; PubMed=10079109;
Kahn M.L., Nakanishi-Matsui M., Shapiro M.J., Ishihara H.,
Coughlin S.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of human genes.";
Nat. Genet. 22:231-238(1999).
                                                                                                                                                                                                                                                                                   Cell 64:1057-1068(1991).
                                                                                                                                                 Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                        Lander B.S.;
Nat. Genet. 23:373-373 (1999).

1- Genet. 23:373-373 (1999).

1- FUNCION: High affinity receptor for activated thrombin coupled to g proteins that estimulate phosphoinositide hydrolysis. May play a role in platelets activation and in vascular development.

1- SUBCELLUIAR LOCATION: Integral membrane protein.

1- TISSUE SPECIFICITY: Platelets and vascular endothelial cells.

1- FTM: A proteolytic cleavage generates a new amino terminus that functions as a terhered ligand.

1- FTM: Phosphorylated; probably mediating desenzitisation prior to the uncoupling and internalization of the receptor.

1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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RGO; GO: 0005887; C: integral to plasma membrane; TAS.

RGO; GO: 0005887; C: integral to plasma membrane; TAS.

RGO; GO: 0005102; F: receptor binding; TAS.

RGO; GO: 0006912; F: throughin receptor activity; TAS.

RGO; GO: 0006919; P: caspase crivation; TAS.

RGO; GO: 0006928; P: cell motility; TAS.

RGO; GO: 0007275; P: development; TAS.

RGO; GO: 0007125; P: invasive growth; TAS.

RGO; GO: 0007125; P: response to wounding; TAS.

RGO; GO: 0007125; P: response to wounding; TAS.

RGO; GO: 0007262; P: STAT protein nuclear translocation; TAS.

RGO; GO: 0007260; P: STAT protein nuclear translocation; TAS.

RGO; GO: 0007260; P: STAT protein nuclear translocation; TAS.

RGO; GO: REPORO, TAM.

RINTENTO; PROMODI; TAM.

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PROSITE; PSS0262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
Blood coagulation; Phosphorylation; Polymorphism; 3D-structure.
Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REMOVED FOR RECEPTOR ACTIVATION. PROTEINASE ACTIVATED RECEPTOR 1.
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CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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EMBL, AF31809; AAK69768.1; -.
EMBL, BC002464; AAH02464.1; -.
EMBL, BC051909; AAH51900.1; -.
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PDB; INRN; 31-MAY-94.
PDB; INRO; 31-MAY-94.
PDB; INRR; 31-MAY-94.
Genew; HGNC:3537; F2R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 41, Last annotation update)
Proteinase activated receptor 1 precursor (PAR-1) (Thrombin receptor).
P2R OR PAR1 OR BTHR12.
Papio hamadryas (Hamadryas baboon).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                             167 DWQFGSELCRFVTAAFYCNMYASILLMTVISIDRFLAVVYPMQSLSWRTLGRASFTCLAI
                                                                       (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                      42;
                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                  Score 228; DB 1; Length 425;
Pred. No. 4.8e-10;
                                                                                                                                                                           L -> V (IN REF. 1).
A -> V (IN REF. 3; AAH02464).
C -> S (IN REF. 3; AAH02464).
41B742A99EEC96AB CRC64;
                                                                                                                                                                                                                                                                                                     46; Mismatches 104; Indels
ASP/GLU-RICH (ACIDIC).
CLEAVAGE (BY THROMBIN).
BY SIMILARITY.
N-LINKED (GLCNAC...) (PR
S-S (Glin GBSNP:5893).
/FTIG=VAR_014167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 425 'AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              323 IICFGPTNVLLIAHYSF 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234 LLCVGPYNASNVASFLY 250
                                                                                                                                                                                                                                 47440 MW;
                                                                                                                                                                                                                                                                  14.4%;
                                                                                                                                                                                                                                                                                                     65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cercopithecinae; Papio.
 60
254
254
35
35
62
75
259
166
                                                                                                                                                                                                                               425 AA;
                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAR1 PAPHA P56488;
                                DISULFID
CARBOHYD
CARBOHYD
                                                                                                     CARBOHYD
CARBOHYD
VARIANT
                                                                                                                                                                                                             CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       178
                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                             CONFLICT
                                                                                                                                                                                                                                                                                      Local
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DARI PAPHA
AC PS648 P
DT 15-JUL
DT 28-JUL
DT 28-JUL
DT 28-ZUL
DT 
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269 YYFSA-----FSAVFFFVPLIISTVCYVSIIRCLSSSTVANRSKKSRALFLSAAVFCIF 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 LYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCSDLLLTVSLPLKAVEALASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167 DWQFGSELCRFVTAAFYCNMYASILLMTVISIDRFLAVVYPMQSLSWRTLGRASFTCLAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71 AWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRPCYSWGVCAAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 WALVLCHIGLV-----FGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAWDPA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 ---SAGPARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHR-RKLRAAWVAGGALLTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
Probable G protein-coupled receptor GPR92.
FOR SPR92 OR GPR93.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
EMBL; AF028727; AAB84191.1; -.
HSSP; P34996; IDDD.
HTGAFPC; PR002076; GPCR_Rhodpsn.
PFR00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00227; GPROTEIN RECEP P1 1; 1.
PROSITE; PS0022; GPROTEIN_RECEP_F1_2; 1.
G-protein couplade receptor; Transmembrane; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.

N-LINKED (GLCNAC. .) (POTENTIAL)

N-LINKED (GLCNAC. .) (POTENTIAL)

N-LINKED (GLCNAC. .) (POTENTIAL)

N-LINKED (GLCNAC. .) (POTENTIAL)
                                                                                                                                                                                                                                                                  REMOVED FOR RECEPTOR ACTIVATION. PROTEINASE ACTIVATED RECEPTOR 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.3%; Score 226; DB 1; Length 425; 25.3%; Pred. No. 6.7e-10; Live 47; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED (GLCNAC. .) (PA 118FC5FB39D4DE2C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
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(GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL
ASP/GLU-RICH (ACIDIC).
CLEAVAGE (BY THROMBIN)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [2]
SEQUENCE FROM N.A.
MEDLINE=21458557; PubMed=11574155;
Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vanti W.B., Arkhitko O.,
Lewis T., Evans J.F., George S.R., O'Dowd B.F.;
"Discovery and mapping of ten novel G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

BEDILINE-22040266, PubMed=12044878;

Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;

"Identification of G protein-coupled receptor genes from the human
                                                                                                                                         White K.E., Evans W.E., O'Riordan J.L.H., Speer M.C., Econs M.J., Lorenz-Depiereux B., Grabowski M., Meitinger T., Strom T.M.; "Autosomal dominant hypophosphataemic rickets is associated with
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterProj IPR000276; GPCR_Rhodpsn.
Pram; PR0001; Thm.1; 1.
PRINTS; PR00237; GPCRHODDPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
                                                                               SEQUENCE FROM N.A.
MEDLINE=20517346; PubMed=11062477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, AJ272207, CAC03715.1; -.
EMBL, AF411112, AAL26483.1; -.
EMBL, AB083600; BAB893313.1; -.
EMBL, BC033571; AAH33571.1; -.
                                                                                                                                                                                                                                                                Nat. Genet. 26:345-348(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'EBS Lett. 520:97-101(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genew; HGNC:13307; GPR92.
MIM; 606926; -.
                                                                                                                                                                                                                                        mutations in FGF23.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene 275:83-91(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                 NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genome sequence
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245 LCFVPYNSTLAVYGLLRSKLVAASVPARDRVRGVLAWWVLAGA-NCVLDPLVXYFSAEG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 KAVEALASGAWPLPASICPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRPC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 YSWGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAW-DPASAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187 RLLPLVLLABBALGFLLPLAAVVYSSGRVFWTLARPDATOSORRRKTVRLLLAN--LVIFL 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LCVGPYNA-----SNVASFLYP---NLGGSWRKLGLITGAWSVVLNPLVTGYLGRG 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 QLSFGLYVAAFALGFPLNVLA----IRGATAHARLRLTPSLVYALNLGCSDLLLTVSLPL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 ---PARPSLSLILFFLPLAITAFCYVGCLRALARSGLT---HRRKLRAAWVAGGALLTLL
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                EXIMALEALLY

CYPOPLASMIC (POTENTIAL).

SYNOPLASMIC (POTENTIAL).

BY SIMILARITY.

N-LINKED (GLCMAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97225799; PubMed=9073069; O'Dowd B.F., Nguyen T., Jung B.P., Marchese A., Cheng R., O'Dowd B.F., Nguyen T., Yorkowski L.F. Jr., Lynch K.R., George S.R.; "Cloning and chromosomal mapping of four putative novel human
                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                           36; Mismatches 141; Indels
                 -LINKED (GLCNAC. . .) (PC
BA35709084BB6D84 CRC64;
                                                                                       2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                       4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                      6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                             3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                   5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                       1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                       13.7%; Score 217.5; DB 1
29.1%; Pred. No. 2.6e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-RDS-2003 (Rel. 41, Last annotation update)
Probable G protein-coupled receptor GPR20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                358 AA
                                                                                                                                                               4 (POTENTIAL)
G PROTEIN RECEP F1 2, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G-protein-coupled receptor genes.";
Gene 187:75-81(1997).
-!- FUNCTION: Orphan receptor.
                                                                                                                                                                                                                                                                                                                                                                       41346 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   283 ----PGLKTVCAART 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       304 FRNTLRGLGTPHRART 319
                                                                                                                                                                                                                                                                                                                                                                                                                                           92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                     372 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
 PROSITE; PS50262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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TRANSMEM
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TRANSMEM
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TRANSMEM
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TRANSMEM
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TRANSMEM
                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                   TRANSMEM
                                                                                                                                                                                                     FRANSMEM
                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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Q99678;
                                    DOMAIN
                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                             DOMAIN
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GP20_HUMAN
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14;

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01-APR-1993 (Rel. 25, Created)
                                                                                                                        Cricetulus.
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TRANSMEM
DOMAIN
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TRANSMEM
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TRANSMEM
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                62 AIFLAGLVINGLALYVFCCRTRAK-TPSVIYTINLVVTDLLVGLSLPTRFAVYYGARGCL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 -- AWPLPASICPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRPCYSWGVCA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIM; 601008; -..
GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0004330; P:G-protein coupled receptor activity; TAS.
GO; GO:0007186; P:G-protein coupled receptor protein signalin. ..; TAS.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PP00001; 7tm 1; 1.
PRINTS; PR00237; GPCRHODPSN.
PROSITE; PS50262; G_PROTEIN_RECRP_F1 1; 1.
PROSITE; PS50262; G_PROTEIN_RECRP_F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.

OG-protein coupled receptor; Promembrane; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 RCAFP-----HVLGYFLNMHCSILFLTCICVDRYLAIVRPEAPAACROPACARAVCA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 AIW----ALVLCHIGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAWDPASAGPARF 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 SLSLLLFFLPLAITAFCYVGCLRALARSGLTH---RRKLRAAWVAGGALLTILLCVGPYN 241
-i- SUBCELLULAR LOCATION: Integral membrane protein.
-i- TISSUB SPECIFICITY: LIVER AND THE BRAIN REGIONS THALAMUS, PUTAMEN, AND CANDATE, BUT NOT IN PRONTAL CORTEX, PONS AND HYPOTHALAMUS.
-i- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 AAFALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCSDLLLTVSLPLK-AVEALASG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (FOTENTIAL).
N-LINKED (GLCNAC. .) (FOTENTIAL)
N-LINKED (GLCNAC. .) (FOTENTIAL)
258066830455B1EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.7%; Score 216.5; DB 1; Length 358; 29.0%; Pred. No. 2.9e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87, Indels
                                                                                                                                                                                                                                                                                                                                                                                         1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              259 6
259 6
275 296
358 CY
16 N'I
38406 MW;
                                                                                                                                                                                             EMBL; U66579; AAC51302.1; -. Genew; HGNC:4475; GPR20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173 FVWLAAGAVTLSVLG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242 ASNVASFLYPNL 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      259 AROVAVALWPDM 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       358 AA;
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PARI_CRILO
ID PARI_CRILO
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AC Q00991, Q60461;
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70
87
108
126
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DOMAIN
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CARBOHYD
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MIM; 60
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428 AA.

PRT;

STANDARD;

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          01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Proteinase activated receptor 1 precursor (PAR-1) (Thrombin receptor)
                                                                                                                                                                                                                                                                                                 PZR OR PARI.
Scriectulus longicaudatus (Long-tailed hamster) (Chinese hamster).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
                                                                                                                                                                                                                                "CDNA cloning and expression of a hamster alpha-thrombin receptor coupled to Ca2+ mobilization."; FEBS Lett. 288:123-128(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; S17148; P1746.
HSSP, P34996; 1DDD.
InterPro; IRR000276; GPCR_Rhodpsn.
PRIMTS; PR000237; GPCRERHODOPSN.
PROSITE; PS00237; GPROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; GPROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Signal; Blood coagulation; Pulmorphiam.
SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REMOVED FOR RECEPTOR ACTIVATION (BY
                                                                                                                                                             TISSUB-Lung;
MEDLINE=91348247; PubMed=1652467;
Rasmussen U.B., Vouret-Craviari V., Jallat S., Schlesinger Y.,
Pages G., Pavirani A. Lecocq J.P., Pouyssegur J.,
Obberghen-Schilling E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEINASE ACTIVATED RECEPTOR 1.
EXTRACELLULAR (POTENTIAL).
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CYTOPLASHIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELUTAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
ASP\GLUGUELITE (POTENTIAL).
POLY-SER.
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLUTAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLUTAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                       SEQUENCE OF 42-428 FROM N.A.
                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                      NCBI_TaxID=10030;
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                                                                                                                                                                                                                                                                                                                                                           177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOI. Pharmacol. 54:541-546(1998).

-!- FUNCTION: RECEPTOR FOR EXTRACELLULAR UDP > ADP = UTP. THE ACTIVITY
OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE A
PHOSPHATIDYLINOSITOL-CALCING SECOND MESSENGER SYSTEM.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      272 YYFSA----FSAVFFLVPLISTICYMSIIRCLSSSSVANRSKKSRALFLSAAVFCVF
                                                                                                                                                                                                                                                                                                                              11 LYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCSDLLLTVSLPLKAVEALASG
                                                                                                                                                                                                                                                                                                                                                                                                                           71 AWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRPCYSWGVCAAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WALVLCHLGLVFGL-----EAPGGWLDHSNTSLGINTPVNGSPVCLEAWDPA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---SAGPARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHR-RKLRAAWVAGGALLTL
(BY SIMILARITY)
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Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Meleagris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               234 LLCVGPYNASNVASFLYPNLGGSWRK-----LGLITGAWSVVLNPLVTGY 278
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
P2Y purinoceptor 3 (P2Y3) (Nucleoside diphosphate receptor)
P2RY3.
                                                                                                                                                                                                                                      Length 428;
                                                                                                                                                                                                                                   13.4%; Score 213; DB 1; Length 428 23.4%; Pred. No. 6.2e-09; ive 53; Mismatches 122; Indels
                 257 BY SIMILARITY.
65 N-LINKED (GLCNAC. . . ) (POTT 178 N-LINKED (GLCNAC. . . ) (POTT 253 N-LINKED (GLCNAC. . . ) (POTT 262 N-LINKED (GLCNAC. . . ) (POTT 264 N-LINKED (GLCNAC. . . ) (POTT 264 N-STING (IN AN ALIBLE) . 384 H -> T (IN REF. 1).
747602 MW, E5492AB2CD877E2F CRC64;
CLEAVAGE (BY THROMBIN)
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                                                                                                                                                                                                                                                                                  68; Conservative
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257
257
253
262
384
384
                                                                                                                                                                                       428 AA;
                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001
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                      DISULFID
CARBOHYD
CARBOHYD
                                                                                                                                      VARIANT
CONFLICT
SEQUENCE
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                                                                                          CARBOHYD
                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                      Query Match
Best Local
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P2Y3 MRLGA
AD 093361,
DT 16-0CT-
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InterPro; IPR000276; GPCR_Rhodpsn. Pfam; PF00001; 7tm_1; 1.

; P34996; 1DDD.

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86 YWPFGDFTCKFVRFQFYTNLHGSILFLTCISVQRYMGICHPLASWHKKKGKKLTWLVCAA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130 IWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAWDP---ASAGPARFSL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            146 VWFIVIAQCLPTFVFASTG------TORNRT-VCYDLSPPDRSASYFPYGITL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13

DARI MOUSE

TO PARI MOUSE

TO 1-APR-1993 (Rel. 25, Created)

DT 01-APR-2094 (Rel. 35, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

B Proteinase activated receptor 1 precursor (PAR-1) (Thrombin receptor).

GN PER OR PARI OF CER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 LYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCSDLLLTVSLPLKAVEALASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71 AWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPL-GYQAFRRPCYSWGVCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=129;
MEDLINE=96379236; PubMed=8784787;
Kahn M.L., 15th i K., Kuo W.L., Piper M., Connolly A., Shi Y.P.,
Kahn M.L., Lin C.C., Coughlin S.R.;
"Conserved structure and adjacent location of the thrombin receptor
and protease-activated receptor 2 genes define a protease-activated
mol. Med. 2:349-357(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                  7 (POTENTIAL).
TATRACELIOLIAR (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 328;
                                                                                                                                                                                                                                                                                                                                                                                                                                 13.1%; Score 208; DB 1; Length 32 30.3%; Pred. No. 1.2e-08; tive 25; Mismatches 105; Indels
                 PROSITE; PS00237; G-PROTEIN RECEP_F1_1; FALSE_NEG.
PROSITE; PS50262; G-PROTEIN_RECEP_F1_2, 1.
G-DXOLtin coupled receptor; Transmembrane; Glycoprotein.
DOMAIN EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Brain;
Coughlin S.R.;
"Cloning of EDNA for the mouse thrombin receptor.";
submitted (OCT-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                          S (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                            B74D49B99C7164A5 CRC64;
                                                                                                                                                                          (POTENTIAL).
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                                                                                                                                                                     3 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                37594 MW;
PRINTS; PR00237; GPCRRHODOPSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 30.3
Matches 67; Conservative
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252
275
275
298
323
172
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57
78
96
1117
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210
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FRANSMEM
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Matches
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Xue J., Jenkins N.A., Gilbert D.J., Copeland N.G., Sadler J.E.;
"Structure and localization of the thrombin receptor gene on mouse chromosome 13.";
Mamm. Genome 7:625-626(1996).
-!- FUNCTION: High affinity receptor for activated thrombin coupled to G proceins that stimulate phosphoinositide hydrolysis.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- PTM: A proteolytic cleavage generates a new amino terminus that functions as a tethered ligand.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                               REMOVED FOR RECEPTOR ACTIVATION (B SIMILARITY).
PROTEINAGE ACTIVATED RECEPTOR 1.
EXTRACELLULAR (POTENTIAL).
1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (POTENTIAL).
EXTRACELLUTAR (POTENTIAL)
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                       EMBL, L03529; AAA40438.1; -.
EMBL, U36757; AAB38308.1; -.
EMBL, U36756; AAB38308.1; JOINED.
EMBL, BC031516; AAA131516.1; -.
EMBL, U55076; AAB00198.1; JOINED.
HSSP; P34966; IDDD.
                                                                                                                                                                                                                 STRAIN=129/Sv;
MEDLINE=96327649; PubMed=8678993;
                                                                                                                                                                                                          SEQUENCE OF 1-74 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       430
107
1133
1142
1162
1181
1203
223
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TRANSMEM
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TRANSMEM
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TRANSMEM
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171 TDWQFGSGMCRFATAAFYGNMYASIMLMTVISIDRFLAVVYPIQSLSWRTLGRANFTCVV 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                231 IWVMAI--MGVVPLLLKEQTTRVPG-----LNITT-----CHDVLSENLMQ 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  270 GFYSYYFSAFSAIFFLVPLIVSTVCYTSIIRCLSSSAVANRSKKSRALFLSAAVFCIFIV 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 GAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRPCYSWGVCAA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 IWALVLCHLGLVFGL-----EAPGGWLDHSNTSLGINTPVNGSPVCLEAWDPASAGPAR 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 LYVAAFALGFPLNVLAIRGATAHARLRL-TPSLVYALNLGCSDLLLTVSLPLKAVEALAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 -----FS-LSLLLFFLPLAITAFCYVGCLRALARSGLTHR-RKLRAAWVAGGALLTLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                      CLEAVAGE (BY THROMBIN) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Panetta R., Greenwood M.T., Warszynska A., Demchyshyn L.L., Day R.,
                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).
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"Modecular cloning and expression of a pituitery somatostatin
receptor with preferential affinity for somatostatin-28.";
Mol. Pharmacol. 42:939-946 (1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    F -> S (IN REF. 1).
G -> Y (IN REF. 1).
R -> G (IN REF. 1).
V -> L (IN REF. 1).
S -> T (IN REF. 1).
S -> T (IN REF. 1).
                         EXTRACELLULAR (POTENTIAL) 5 (POTENTIAL).
                                                                                                                                                                              ASP/GLU-RICH (ACIDIC).
POLY-PRO.
                                                                                                                 6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                     (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.1%; Score 208; DB 1; 25.1%; Pred. No. 1.5e-08;
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01-FRE-1995 (Rel. 31, Last sequence update)
110-CTZ-2003 (Rel. 42, Last annotation update)
Somatostatin receptor type 5 (855R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45; Mismatches
                                                                                     CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Pituitary;
MEDLINE=94195267; PubMed=7908405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE=Pituitary;
MEDLINE=93125499; PubMed=1362243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   365 S
47790 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 330 CFGPTNVLLIVHYLF 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarion hes 64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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365
430 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REVISIONS
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CONFLICT
CONFLICT
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SEQUENCE
                         DOMAIN
TRANSMEM
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TRANSMEM
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201 ITYTSVLGFFGPLLVICLCYLLIVVKVKAAGMRVGSSRRRRSBPKVTRMVVVVVLVFVGC 260
                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A23669; A23669.
PIR; JQ1231; JQ1231.
Interpro; IPRO000276; GPCR_Rhodpsn.
Pfam; PPO0001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Neutrophils;
MEDLINE=92148149; PubMed=1737938;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M74240; AAA31375.1; -. EMBL; M58021; AAA31377.1; -. EMBL; M82873; AAA31376.1; -.
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M82873; AAA31376.1;
                                                                                                                                                                                STANDARD;
                                                                                   289 CAARTQG 295
                                                                                                              320 CLRRGYG 326
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9986;
                                                                                                                                                                               IL8A RABIT
P21109;
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                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43 LYLLVCTVGLSGNTLVIYVVLRHAKMK-TVTNVYILNLAVADVLFMLGLPFLATQNAVVS 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 AWPLPASLCPVF----AVAHFFPLYAGGGFLAALSAGRYLGAAFFLGYQAFRRPCYSWGV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102 YWPFGSFLCRLVMTLDGINQFTSIFC----LMVMSVDRYLAVVHPLRSARWRRPRVAKMA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127 CAAIWAL-VLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAW-DPASAGPARF 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --SISILLFFLFLAITAFCYVGCLRALARSGL---THRRKLRAAWVAGGALLTLLLCVG- 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 LYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCSDLLLTVSLPLKAVEALASG 70
Niznik H.B., Srikant C.B., Patel Y.C.;
"Molecular cloning, functional characterization, and chromosomal localization of a human somatostatin receptor (somatostatin receptor type 5) with preferential affinity for somatostatin-28.",
Mol. Pharmacol. 45:417-427(1994).
-!- FUNCTION: Receptor for somatostatin-28. The activity of this receptor is mediated by G proteins which inhibit adenylyl cyclase.-!- SUBCELIULAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: Prominent in the pituitary and small intestine. Low levels in islets and spleen. Not detected in kidney, pancreas, cerebellum, or cortex.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.0%; Score 205.5; DB 1; Length 363; 25.4%; Pred. No. 1.9e-08; ive 49; Mismatches 135; Indels 45.
                                                                                                                                                                                                                                                                                                                                              Interproj IPR000276; GPCR_Rhodpsn.
Pfam; PR0001; 7tm 1; 1.
PRINTS; PR00237; GPCRHODOPSN.
PROSITE; PS00237; G_PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G_PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Lipoprotein; Palmitate.
DOMAIN.

SETRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL)
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                                                                                                                                                                                                                                                                                  EMBL; L04535; AAA17029.1; --
EMBL; U01152; AAC09011.1; --
EMBL; X74628, CAA52825.1; --
BTR; I57940; I57940.
HSSP; P02699; IF88.
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TRANSMEM
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239 --PYNASNVASFLY----PNLGGSWRKLGLITGAWSVVLNPLVTGYLG---RGPGLKTV 288
                                          261 WLPFFIVNIVNLAFTLPEEPTSAGLYFFVVVLSYANSCA-NPLLYGFLSDNFRQSFRKVL 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=Albino; TISSUE=Neutrophils;
MEDLINE=91056034; PubMed=1700779;
Thomas K.M., Pyun H.Y., Navarro J.;
"Molecular cloning of the fMet-Leu-Phe receptor from neutrophils.";
J. Biol. Chem. 265:20061-20064 (1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLUIAR LOCATION: Integral membrane protein.
TISSUB SPECIFICITY: Neutrophils.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CAUTION: Was originally (Ref.2) thought to be the receptor fMet-Leu-Phe (N-formyl peptide receptor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryccolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=91378994; PubMed=1898400; Beckmann M.P., Munger W.E., Kozlosky C., Vanden Bos T., Price V., Lyman S., Gerard N.P., Cerretti D.P.; "Grard C., Cerretti D.P.; "Molecular characterization of the interleukin-8 receptor."; Biochem. Biophys. Res. Commun. 179:784-789(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lee J., Kuang W.-J., Rice G.C., Wood W.I.; "Characterization of complementary DNA clones encoding the rabbit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High affinity interleukin-8 receptor A (IL-8R A) (CXCR-1) ILBRA OR CXCR1.
                                                                                                                                                                                                                                                                                                                                                                                                                  355 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1991 (Rel. 17, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation updat
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48 VVIYALVFLESLIGNSLVMLVLYSRSNRSVTDVYLLALAMADLLFALTMPIWAVS--KE 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 GAWPLPASLCPVFAVAHFPPLYAGGGFLAALSAGRYLGAAFPLGYOAFRRPCYSWGVCAA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      106 KGWIFGTPLCKVVSLVKEVNFYSGILLIACISVDRYLAIVHATRTLIQKRHLVKF-ICLG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 IWALVLCHIGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAWDPASAGPARFSLSLL 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165 IWALSLI-LSLPFFLFRQ------VFSPNNSSPVC---YBDLGHNTAKWRMVLR 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190 L----FFLPLAITAFCYVGCLRAL--ARSGLTHRRKLRAAWVAGGALLTLLLCVGPYN 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------RSNVASFLYPNLGGSWRKLGLITGAWSVULN 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 VAAPALGPPLNVLA---IRGATAHARLRLTPSLVYALNIGCSDLLLTVSLPLKAVEALAS 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83;
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PAFCPDHAYLGRLQGRRLDFR (IN REF. 2).
HA -> QS (IN REF. 2).
R -> C (IN REF. 2).
B -> EL (IN REF. 2).
FE49ACB9D1E0F21 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Match 12.9%; Score 204.5; DB 1; Length 355; Local Similarity 25.8%; Pred. No. 2.3e-08; es 83; Conservative 39; Mismatches 117; Indels 83
G PROTEIN RECEP F1 1; 1.

G PROTEIN RECEP F1 2; 1.

receptor; Transmembrane; Glycoprotein;
                                                                                                                                            1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                    4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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